

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 09:32:08 ; Search time 44 Seconds
(without alignments)
225.235 Million cell updates/sec

Title: US-09-856-199-3
Perfect score: 506
Sequence: 1 KRCINQLLCKLPDSELA...EASASXXKQAKKXEPSPN 103

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	479	94.7	381	1 A47327	selenoprotein P pr
2	329.5	65.1	380	2 T10442	selenoprotein P pr
3	309.5	61.2	385	1 OMRTSP	selenoprotein P pr
4	73.5	14.5	868	2 A30817	serendipity (sry h
5	71.5	14.1	419	2 A40728	microphthalmia-ass
6	67.5	13.3	419	2 T38024	MITF protein - hum
7	66.5	13.1	1002	2 T02488	hypothetical prote
8	66	13.0	271	2 GB3016	hypothetical prote
9	65.5	12.9	142	2 AB0138	TolR colicin impor
10	65.5	12.9	604	2 S88419	apoptosis inhibito
11	65	12.8	1008	2 T30544	major surface glyc
12	64.5	12.7	86	1 TNLJND	trans-activating t
13	64	12.6	95	1 FERFNC	ferredoxin [2Fe-2S
14	63.5	12.5	716	1 A40332	macrophage-stimula
15	63.5	12.5	770	2 T22944	hypothetical prote
16	63.5	12.5	784	2 T22939	hypothetical prote
17	63.5	12.5	900	2 T41607	probable vacuolar
18	62.5	12.4	1009	2 S64734	retrovirus-related
19	62	12.3	419	2 A59414	metalloproteinase
20	62	12.3	739	2 HB5245	vpl like protein l
21	62	12.3	739	2 T05163	hypothetical prote
22	61.5	12.2	618	2 T44595	alcaligin synthesi
23	61.5	12.2	639	2 A32545	protein kinase C (
24	61	12.1	258	2 B84455	En/Spm-like transp
25	61	12.1	273	2 T16246	hypothetical prote
26	61	12.1	700	2 T77463	luteinizing hormon
27	61	12.1	700	2 A49744	lutropin-choriogon
28	60.5	12.0	383	2 F69018	formate dehydrogen
29	60.5	12.0	1423	1 S27941	serum albumin - se

RESULT 1
A47327
selenoprotein P precursor [validated] - human
C/Species: Homo sapiens (man)
C/Date: 21-Sep-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C/Accession: A47327; S42752
R/Hill, K.E.; Lloyd, R.S.; Burk, R.F.
Proc. Natl. Acad. Sci. U.S.A. 90, 537-541, 1993
A/Title: Conserved nucleotide sequences in the open reading frame and 3' untranslated re
A/Reference number: A47327; MUID:93133823; PMID:8421687
A/Accession: A47327
A/Molecule type: mRNA
A/Residues: 1-381 <HIL>
A/Cross-references: UNIPROT:P49908; GB:Z11793; NID:G36425; PIDN:CAA77836.1; PID:G2654365
A/Experimental source: heart and liver
A/Note: In Genbank entry HSSELP, release 117.0, PIDN:CAA77836.1, the selenocysteine UGA
R/Akesson, B.; Bellew, T.; Burk, R.F.
Biochim. Biophys. Acta 1204, 243-249, 1994
A/Title: Purification of selenoprotein P from human plasma.
A/Reference number: S42752; MUID:94191007; PMID:8142465
A/Accession: S42752
A/Molecule type: protein
A/Residues: 20-27, 'X', 29-33 <AKE>
A/Note: mature forms of 55K and 61K were detected in plasma; the protein was shown to cor
C/Genetics:
A/Gene: GDB:SEPP1; SLNP
A/Cross-references: GDB:138278; OMIM:601484
A/Map position: 5q31-5q31
C/Function:
A/Description: may act as a free-radical scavenger
C/Superfamily: selenoprotein P
C/Keywords: extracellular protein; glycoprotein; heparin binding; liver; plasma; selenoc
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-381/Product: selenoprotein P #status experimental <MAT>
F/46,83,119,128,338/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/59,300,318,330,345,352,367,369,376,378/Modified site: selenocysteine #status predicted

Query Match		94.7%	Score 479;	DB 1;	Length 381;
Best Local Similarity		91.3%	Pred. No. 9.1e-45;		
Matches		94;	Conservative	0;	Mismatches
				9;	Indels
				0;	Gaps
				0;	
Qy	1	KRCINQLLCKLPDSELA	PRSCCHRLIFEKTSALTQCKENLPSLCSCQGLRAEN	60	
Db	279	KRCINQLLCKLPDSELA	PRSCCHRLIFEKTSALTQCKENLPSLCSCQGLRAEN	338	
Qy	61	ITESCQRLPPAAQISQ	LIPTASASXXKQAKKXEPSPN	103	
Db	339	ITESCQRLPPAAQISQ	LIPTASASCRCKNQAKKCEPSPN	381	

RESULT 2
T10442

selenoprotein P precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C/Accession: T10442
R/Steinert, P.; Ahrens, M.; Gross, G.; Flohe, L.
BioFactors 6, 311-319, 1997
A/Title: cDNA and deduced polypeptide sequence of a mouse selenoprotein P.
A/Reference number: 217017; MUID:97434516; PMID:9288402
A/Accession: T10442
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-380 <STE>
A/Cross-references: EMBL:X99807; NID:g1495998; PIDN:CAA68140.1; PID:g1495999
C/Genetics:
A/Gene: selp
C/Superfamily: selenoprotein P
C/Keywords: extracellular protein; selenocysteine

Query Match 65.1%; Score 329.5; DB 2; Length 380;
Best Local Similarity 71.3%; Pred. No. 1.9e-28;
Matches 72; Conservative 9; Mismatches 19; Indels 1; Gaps 1;

Qy 3 CINQLLCKLPDSELA PRSXCCHRH LIFKTSAITXQCKENLPSCSXQGLRAEENIT 62
Db 281 CINQLLCKLSBSGAATSSCCCHRH LIFKTSAGTAXQCAENLPSCSXQGLFAEKEVT 340

Qy 63 ESCQXRLPPAAQXQISQQLIPTASAXRXKXQKXEXPNS 103
Db 341 ESCQCRSPAAQXQ-NQPNVPEANPNKXNDQTRKXKXHSN 380

RESULT 3
QWRTSP
selenoprotein P precursor [validated] - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: A40380; B40380; S68322
R/Hill, K.E.; Lloyd, R.S.; Yang, J.G.; Read, R.; Burk, R.F.
J. Biol. Chem. 266, 10050-10053, 1991
A/Title: The cDNA for rat selenoprotein P contains 10 TGA codons in the open reading frame
A/Reference number: A40380; MUID:91244760; PMID:2037562
A/Accession: A40380
A/Molecule type: mRNA
A/Residues: 1-385 <HIL>
A/Cross-references: UNIPROT:P25236; GB:M63574; NID:g206893; PIDN:AAA42129.1; PID:g206894
A/Accession: B40380
A/Molecule type: protein
A/Residues: 20-41;267-287;316-327 <HI2>
R/Chittum, H.S.; Himeno, S.; Hill, K.E.; Burk, R.F.
Arch. Biochem. Biophys. 325, 124-128, 1996
A/Title: Multiple forms of selenoprotein P in rat plasma.
A/Reference number: S68322; MUID:96140605; PMID:8554336
A/Accession: S68322
A/Molecule type: protein
A/Residues: 20-27 <CHI>
C/Superfamily: selenoprotein P
C/Keywords: extracellular protein; glycoprotein; heparin binding; liver; plasma; selenocysteine
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-385/Product: selenoprotein P #status experimental <MAT>
F/59,264,335,357,371,373,380,382/Modified site: selenocysteine #status predicted
F/83,174,188,370,375/Binding site: carboxylate (Asn) (covalent) #status predicted
F/282,323/Modified site: selenocysteine #status experimental

Query Match 61.2%; Score 309.5; DB 1; Length 385;
Best Local Similarity 66.3%; Pred. No. 3e-26;
Matches 63; Conservative 6; Mismatches 25; Indels 1; Gaps 1;

Qy 3 CINQLLCKLPDSELA PRSXCCHRH LIFKTSAITXQCKENLPSCSXQGLRAEENIT 62
Db 286 CINQLLCKLSBSGAATSSCCCHRH LIFKTSAGTAXQCAENLPSCSXQGLFAEKEVT 345

Qy 63 ESCQXRLPPAAQXQISQQLIPTASAXRXKXQKXEXPNS 97

Db 346 ESCQCRSPPAACH-SQHVSPTEASPNCSNNKTKK 379

RESULT 4
A30817
serendipity (sry h-1) locus protein - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C/Accession: A30817
R/Vincent, A.; Keizlarova-Lepesant, J.; Segalat, L.; Yanicostas, C.; Lepesant, J.A.
Mol. Cell. Biol. 8, 4459-4468, 1988
A/Title: sry h-1, a new Drosophila melanogaster multifingered protein gene showing mater
A/Reference number: A30817; MUID:89039875; PMID:3141791
A/Accession: A30817
A/Molecule type: DNA
A/Residues: 1-868 <VIN>
A/Cross-references: UNIPROT:P15619; GB:M23391; NID:g340903; PID:g387593
C/Genetics:
A/Gene: FlyBase:wdn
A/Cross-references: FlyBase:FBgn0005642
A/Introns: 338/2; 740/1
C/Keywords: DNA binding; transcription regulation; zinc finger

Query Match 14.5%; Score 73.5; DB 2; Length 868;
Best Local Similarity 28.6%; Pred. No. 3.8; Mismatches 29; Indels 27; Gaps 4;
Matches 26; Conservative 9

Qy 27 RHLIFKTSAITXQCKENLPSCSXQGLRAEENITESCO--XRLPPAAQXQISQQLIPTE 84
Db 491 RHKVDHKTGEHL-----ENIPSYCS-----KKSTTKAKAAAAAASSAVNPNE 539

Qy 85 ASASRXK-----NQAKXEXP 101
Db 540 LSASSELKAKANLTSTAAPAKQAKKKQF 570

RESULT 5
A40728
microphthalmia-associated transcription factor mi - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C/Accession: A40728; A48021; I49245; S36645
R/Hodgkinson, C.A.; Moore, K.J.; Nakayama, A.; Steingrimsson, E.; Copeland, N.G.; Jenkins
Cell 74, 395-404, 1993
A/Title: Mutations at the mouse microphthalmia locus are associated with defects in a ger
A/Reference number: A40728; MUID:93345026; PMID:8343963
A/Accession: A40728
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-419 <HOD>
A/Cross-references: UNIPROT:Q08874; GB:Z23066; NID:g396739; PIDN:CAA80600.1; PID:g396740
R/Hughes, M.J.; Lingrel, J.B.; Krakowsky, J.M.; Anderson, K.P.
J. Biol. Chem. 268, 20687-20690, 1993
A/Title: A helix-loop-helix transcription factor-like gene is located at the mi locus.
A/Reference number: A48021; MUID:94012591; PMID:8407885
A/Accession: A48021
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 238-286 <HUG>
A/Cross-references: GB:L22958
R/Steingrimsson, E.; Moore, K.J.; Lamoreux, M.L.; Ferre-D'Amare, A.R.; Burley, S.K.; San
Nature Genet. 8, 256-263, 1994
A/Title: Molecular basis of mouse microphthalmia (mi) mutations helps explain their devel
A/Reference number: I49244; MUID:95179171; PMID:7874168
A/Accession: I49245
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-16 <RES>
A/Cross-references: EMBL:U19875; NID:g642572; PIDN:AAC52156.1; PID:g642573
C/Genetics:
A/Gene: mi
C/Keywords: DNA binding; transcription factor

A;Cross-references: GB:AE002093; NID:g3420054; PIDN:NAC31855.1; GSPDB:GN00139
C;Genetics:
A;Gene: F23F1.11; At2g29970
A;Map position: 2
A;Introns: 387/2; 467/3

Query Match 13.1%; Score 66.5; DB 2; Length 1002;
Best Local Similarity 34.8%; Pred. No. 25;
Matches 16; Conservative 8; Mismatches 15; Indels 7; Gaps 2;

QY 10 KLPTDSBL--APRSXCCHCRH---LIFEKTGSAITXOCKENLPS 48
|||::|||::|||::|||::|||::|||
Db 406 RIPSSSNQTLPRCHLCNEKYEQEVTAFAKSGMIDDCCSEKLPS 451
|||::|||::|||::|||::|||::|||

RESULT 8
G83016
hypothetical protein PA5027 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G83016
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brj
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.-; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: AB2950; MUID:20437337; PMID:10984043
A;Accession: G83016
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-271 <STO>
A;Cross-references: UNIPROT:Q9HUE2; GB:AE004916; GB:AE004091; NID:g9951315; PIDN:AAG0841;
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA5027

Query Match 13.0%; Score 66; DB 2; Length 271;
Best Local Similarity 26.4%; Pred. No. 8.3;
Matches 19; Conservative 13; Mismatches 30; Indels 10; Gaps 3;

QY 11 LPTSELAPRSXCCHRLIFEKTGSAITXOCKENLPSCXQGLRAEENITESCXRLP 70
|||::|||::|||::|||::|||::|||
Db 157 LPVEADL-----HALH-VFESPPDGVGLPRQNAHLATQAGL--IFQLLSDEQERLP 206
|||::|||::|||::|||::|||::|||

QY 71 PAAXQIQSOQLIP 82
|||::|||::|||
Db 207 GVGPQLSHEVVP 218
|||::|||::|||

RESULT 9
AB0138
ToLR colicin import membrane protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0138
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F
ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0138
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-142 <CUR>
A;Cross-references: UNIPROT:Q8ZGZ3; GB:AL590842; PIDN:CAC89965.1; PID:g15979189; GSPDB:GN
C;Genetics:
A;Gene: tolR
C;Superfamily: tolR protein

Query Match 12.9%; Score 65.5; DB 2; Length 142;
Best Local Similarity 25.0%; Pred. No. 5.1;
Matches 21; Conservative 11; Mismatches 27; Indels 25; Gaps 3;

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Qy 29 LIFEKTSATXQCKENLPSCXQGLRAENITESCQXRLPPAAXQIS----- 77
Db 30 LIFWATAPILITQSEVNLPDTSKTVSSDDN-----PPVIVEVSGQYTVVVDH 80

Qy 78 --QQLIPTE---ASASXXKQAK 96
Db 81 ORMELLPEQVVAEAQARLKNPK 104

RESULT 10
S68449
A:Title: apoptosis inhibitor hiap-1 - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S68449
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68449
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-604 <LIS>
A:Cross-references: UNIPROT:Q13489; EMBL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g118
C:Function:
C:Keywords: apoptosis; zinc finger
F:553-597/Domain: RING finger homology <RNG>

Query Match 12.9%; Score 65.5; DB 2; Length 604;
Best Local Similarity 27.7%; Pred. No. 20;
Matches 23; Conservative 11; Mismatches 42; Indels 7; Gaps 3;

Qy 24 CHCRHLIFE--KTGSATXQCKENLPSCXQGLRAENITESCQXRLPPAAXQISQOLI 81
Db 66 CFCGGLMDLNWKRGDSPTEKHKLKYPSCRFVQSLNVNLEATSOPTFPSSVTHSTHLL 125

Qy 82 P-TEASASXXKQAKKXKXPSN 103
Db 126 PGTENSGYFR---GSYSNSPSN 144

RESULT 11
T30544
A:Title: major surface glycoprotein - Pneumocystis carinii (fragment)
C:Species: Pneumocystis carinii
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001
C:Accession: T30544
R:Mei, Q.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A.
Infect. Immun. 66, 4268-4273, 1998
A:Title: Characterization of major surface glycoprotein genes of human Pneumocystis car
A:Reference number: 217905; MUID:98380374; PMID:9712777
A:Accession: T30544
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1008 <MEI>
A:Cross-references: EMBL:AF033212; NID:g3560520; PID:g3560521; PIDN:AAC34975.1
C:Genetics:
C:Superfamily: Pneumocystis carinii major surface glycoprotein MSG100

Query Match 12.8%; Score 65; DB 2; Length 1008;
Best Local Similarity 21.7%; Pred. No. 37;
Matches 26; Conservative 23; Mismatches 47; Indels 24; Gaps 5;

Qy 1 KRCINQLLCKLPTDSELA PRSC-----CHCRHLIFEKTSATXQCKENLPSC----- 48
Db 697 KRKVELDALKVELQNLNRRNKCSALERYCT-ILKNVSDSSINSLCKDNKTESKTKTDN 755

Qy 49 -----LCSXQGLRAENITESCQXRLPPAAXQISQOLIPTASASXXKQAKKXKXPSN 103
Db 756 EVRKKLC-----LKLVEVEQCC--KMLPAELHEHEKDLKDDFTFEKLKQAKETMKNKN 809
```

RESULT 12

TNLJND

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate p
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JQ0071
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989

A:Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immunoc
A:Reference number: JQ0065; MUID:90034200; PMID:2806917
A:Accession: JQ0071
A:Molecule type: DNA
A:Residues: 1-86 <SPI>

A:Cross-references: UNIPROT:P18804; GB:M27323; NID:g328154; PIDN:AAA44866.1; PID:g328155

C:Genetics:

A:Gene: tat

C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS; immunodeficiency; transcription

Query Match 12.7%; Score 64.5; DB 1; Length 86;

Best Local Similarity 25.8%; Pred. No. 4.1;

Matches 23; Conservative 7; Mismatches 36; Indels 23; Gaps 3;

Qy 12 PTDSEL-----APRSXC--CHCRHLIFEKTSATXQCKENLPSCXQGLRAENI 61

Db 3 PVDNLESWNHPSQPRACNKCKCKCVCVCFIT-----KGLGISYGR 49

Qy 62 TSCQXRLPPAAXQISQOLIPTASASXR 90

Db 50 KKRQRKPPQGDQAHQVPIPEQPSQSR 78

RESULT 13

FERENC

ferredoxin [2Fe-2S] - Rhodobacter capsulatus

N:Alternate names: ferredoxin IV; plant-type ferredoxin

C:Species: Rhodobacter capsulatus

C>Date: 31-Dec-1990 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004

C:Accession: S08393; B39857; A39519; S39897

R:Saeki, K.; Miyatake, Y.; Young, D.A.; Marrs, B.L.; Matsubara, H.

Nucleic Acids Res. 18, 1060, 1990

A:Title: A plant-ferredoxin-like gene is located upstream of ferredoxin I gene (fdxN) of

A:Reference number: S08393; MUID:90192101; PMID:2315024

A:Accession: S08393

A:Molecule type: DNA

A:Residues: 1-95 <SA>

A:Cross-references: UNIPROT:P16022; EMBL:X51316; NID:g46141; PIDN:CAA35698.1; PID:g46142

R:Saeki, K.; Suettsugu, Y.; Tokuda, K.; Miyatake, Y.; Young, D.A.; Marrs, B.L.; Matsubara,

J. Biol. Chem. 266, 12889-12895, 1991

A:Title: Genetic analysis of functional differences among distinct ferredoxins in Rhodosp

A:Reference number: A39857; MUID:91302301; PMID:2071578

A:Accession: B39857

A:Molecule type: DNA

A:Residues: 1-95 <SA2>

A:Cross-references: GB:X51316; GB:S42008; NID:g46141; PIDN:CAA35698.1; PID:g46142

R:Grabau, C.; Schatt, E.; Jouanneau, Y.; Vignais, P.M.

J. Biol. Chem. 266, 3294-3299, 1991

A:Title: A new [2Fe-2S] ferredoxin from Rhodobacter capsulatus. Coexpression with a 2[4Fe

A:Reference number: A39519; MUID:91131639; PMID:1847145

A:Accession: A39519

A:Molecule type: DNA

A:Residues: 1-95 <GRA>

A:Cross-references: GB:M59855; GB:J05743; NID:g151915; PIDN:AAA26109.1; PID:g151916

R:Schmehl, W.; Jahn, A.; Meyer zu Vilsendorff, A.; Hennecke, S.; Masepohl, B.; Schuppier,

Mol. Gen. Genet. 241, 602-615, 1993

A:Title: Identification of a new class of nitrogen fixation genes in Rhodobacter capsulat

A:Reference number: S39892; MUID:94088454; PMID:8264535

A:Accession: S39897

A:Status: preliminary

A:Molecule type: DNA

[illegible]

RESULT 14

A40332

macrophage-stimulating protein 1 precursor - mouse

N/Alternate names: hepatocyte growth factor-like protein

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

C/Accession: A40332; B40332

R/Begen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.

B/Biochemistry 30, 9781-9791, 1991

A/Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth factor

A/Reference number: A40332; MUID:92002017; PMID:1832957

A/Accession: A40332

A/Molecule type: DNA

A/Residues: 1-716 <DEG>

A/Cross-references: UNIPROT:P26928; GB:W74180; NID:G193831; PIDN:AAA50166.1; PID:G193832

A/Accession: B40332

A/Molecule type: mRNA

A/Residues: 1-18, 'P', 20-716 <DEG2>

A/Cross-references: GB:W74181; NID:G193833; PIDN:AAA50167.1; PID:G193834

C/Genetics:

A/Introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 477/1

C/Complex: disulfide-bonded heterodimer of chains derived from the same precursor

C/Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolc

C/Keywords: duplication; glycoprotein; growth factor; kringle

F/1-31/Domain: signal sequence #status predicted <SIG>

F/19-488,489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>

F/19-483/Domain: alpha chain #status experimental <ACH>

F/110-186/Domain: kringle homology <KR1>

F/191-268/Domain: kringle homology <KR2>

F/292-370/Domain: kringle homology <KR3>

F/379-457/Domain: kringle homology <KR4>

F/484-711/Domain: beta chain #status experimental <BCH>

F/489-709/Domain: trypsin homology <TRY>

F/172,173,305,620/Binding site: carboxylate (Asn) (covalent) #status predicted

```

Query Match      12.5%; Score 63.5; DB 1; Length 716;
Best Local Similarity 29.6%; Pred. No. 39;
Matches 21; Conservative 13; Mismatch 26; Indels 11; Gaps 5;

Qy      1 KRCINQLLCKLPDTSELAPRSXCCHC--RHILPEKTSAITXQCKENLPSLCSXQGLRAE 58
      | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      149 KNGLEENFCRNP-DGD--PRGPMCYTTNRSVRFQSCG---IKTCREAVCVLNCNGEDYRGE 202

Qy      59 ENITES---CQ 66

Db      203 VDVTESGRECQ 213
      : : | | | |

```

RESULT 15
T22944

hypothetical protein F58G11.1b - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22944

R;Percy, C.
submitted to the EMBL Data Library, October 1996

A;Reference number: Z19640
A;Accession: T22944
A;Status: preliminary; translated from GB/EMBL/DDBB
A;Molecule type: DNA
A;Residues: 1-770 <WIL>
A;Cross-references: UNIPROT:Q9XVL7; EMBL:Z81094; PIDN:CABO3156.1; GSPDB:GN00023
A;Experimental source: clone F58G11
C;Genetics:
A;Gene: CESP:F58G11.1b
A;Map position: 5
A;Introns: 44/2; 184/3; 360/2; 708/3; 743/3

Query Match 12.5%; Score 63.5; DB 2; Length 770;
Best Local Similarity 32.8%; Pred. No. 42;
Matches 20; Conservative 9; Mismatches 19; Indels 13; Gaps 3;

Qy 45 NLSFLCSXQGLRA-----EENITE-----SCQRLPPAAHQISQOL-IPTASASXR X 91
:| | | :||| :| | :| | :| | :| | :| | :| |
Db 315 DLQSACRAGMRGAIVSGVEERLKQLVQWLSELDKVPALLLSRTL YLPPEVSVFPDRL 374

Qy 92 K 92
|
Db 375 K 375

Search completed: April 15, 2005, 10:11:22
Job time : 47 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2005, 09:30:33 ; Search time 183 Seconds

(without alignments)
288.219 Million cell updates/sec

Title: US-09-856-199-3

Perfect score: 506

Sequence: 1 KRCINQLLCKLPTDSELAPR.....EASASRXKNQAKKXEPSN 103

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	479	94.7	381	1 SELP HUMAN	P49908 homo sapien
2	479	94.7	381	2 Q6PD59	Q6pd59 homo sapien
3	479	94.7	381	2 Q6PI87	Q6pi87 homo sapien
4	479	94.7	381	2 Q6PIF9	Q6pif9 homo sapien
5	475	93.9	381	2 Q6PI43	Q6pi43 homo sapien
6	362.5	71.6	386	2 Q9NZH6	Q9nzh6 bos taurus
7	353.5	69.9	402	1 SELP BOVIN	P49907 bos taurus
8	322.5	63.7	380	1 SELP MOUSE	P70274 mus musculus
9	321.5	63.5	380	2 Q8OT08	Q8ot08 mus musculus
10	320.5	63.3	380	2 Q8OUF3	Q8ouf3 mus musculus
11	320.5	63.3	380	2 Q6PKE7	Q6pke7 mus musculus
12	309.5	61.2	385	1 SELP RAT	P25236 rattus norv
13	135.5	26.8	367	1 SEPA BRARE	Q98sv1 brachydanio
14	135.5	26.8	367	2 Q6P3K0	Q6p3k0 brachydanio
15	79.5	15.7	5183	1 PCLO HUMAN	Q9y6v0 homo sapien
16	74.5	14.7	86	2 Q8JEB8	Q8jeb8 human immun
17	73.5	14.5	868	1 SRVC DROME	P15619 drosophila
18	73.5	14.5	869	2 Q9VAT4	Q9vat4 drosophila
19	73	14.4	99	1 TAT HVIEL	P04611 human immun
20	71.5	14.1	361	2 Q8CGY4	Q8cgy4 mus musculus
21	71.5	14.1	377	2 Q70241	Q70241 mesocricetu
22	71.5	14.1	526	1 MTFP MOUSE	Q08874 mus musculus
23	71	14.0	1155	2 Q8C8W5	Q8c8w5 mus musculus
24	71	14.0	1407	2 Q69ZL1	Q69z11 mus musculus
25	69	13.6	946	2 Q6DCM5	Q6dcms xenopus lae
26	68.5	13.5	358	1 VEGD MOUSE	P97946 mus musculus
27	68	13.4	949	2 Q6DEX9	Q6dex9 xenopus tro
28	67.5	13.3	123	2 Q6Y908	Q6y908 human immun
29	67.5	13.3	354	1 VEGD HUMAN	Q43915 homo sapien
30	67.5	13.3	408	2 Q6UUT7	Q6uut7 canis famil
31	67.5	13.3	419	2 Q21563	Q21563 caenorhabdi

32	67.5	13.3	419	2 Q864F3	Q864f3 canis famil
33	67.5	13.3	526	1 MTFP HUMAN	Q75030 homo sapien
34	67.5	13.3	1624	2 Q9H4C9	Q9h4c9 homo sapien
35	67.5	13.3	1790	2 Q96PH8	Q96ph8 homo sapien
36	67.5	13.3	1791	2 Q9BXP8	Q9bxp8 homo sapien
37	67	13.2	102	2 Q9QSR9	Q9qsr9 human immun
38	67	13.2	474	2 Q9IBH7	Q9ibh7 coturnix co
39	67	13.2	612	2 Q8UVG0	Q8uvg0 bothrops er
40	67	13.2	963	2 Q7PCR4	Q7pcr4 anopheles g
41	67	13.2	1334	2 Q7Q2B2	Q7q2b2 anopheles g
42	66.5	13.1	1002	2 Q80875	Q80875 arabidopsis
43	66.5	13.1	1002	2 Q94BS5	Q94bs5 arabidopsis
44	66.5	13.1	1408	2 Q24341	Q24341 drosophila
45	66.5	13.1	1436	2 Q9VX60	Q9vx60 drosophila

ALIGNMENTS

RESULT 1

ID	SELP HUMAN	STANDARD;	PRT;	381 AA.
AC	P49908;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Selenoprotein P precursor (Sep).			
GN	Name=SEPP1; Synonyms=SELP;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RP	TISUE=Heart and Liver;			
RC	MEDLINE=93133823; PubMed=8421687;			
RA	Hill K.E., Lloyd R.S., Burk R.F.;			
RT	"Conserved nucleotide sequences in the open reading frame and 3' untranslated region of selenoprotein P mRNA.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 90:537-541(1993).			
RN	[2]			
RP	PARTIAL SEQUENCE.			
RA	MEDLINE=94191007; PubMed=8142465;			
RA	Aakesson B., Bellew T., Burk R.F.;			
RT	"Purification of selenoprotein P from human plasma.";			
RL	Biochim. Biophys. Acta 1204:243-249(1994).			
RN	[3]			
RP	CHARACTERIZATION.			
RA	MEDLINE=98413836; PubMed=9735174; DOI=10.1006/abbi.1998.0809;			
RA	Mostert V., Lombek I., Abel J.;			
RT	"A novel method for the purification of selenoprotein P from human plasma.";			
RL	Arch. Biochem. Biophys. 357:326-330(1998).			
RN	[4]			
RP	CHARACTERIZATION.			
RA	MEDLINE=20239644; PubMed=10775431; DOI=10.1006/abbi.2000.1735;			
RA	Mostert V.;			
RT	"Selenoprotein P: properties, functions, and regulation.";			
RL	Arch. Biochem. Biophys. 376:433-438(2000).			
RN	[5]			
RP	REVIEW.			
RA	MEDLINE=95017128; PubMed=7931697;			
RA	Burk R.F., Hill K.E.;			
RT	"Selenoprotein P: A selenium-rich extracellular glycoprotein.";			
RL	J. Nutr. 124:1891-1897(1994).			
CC	-!- FUNCTION: Might be responsible for some of the extracellular antioxidant defense properties of selenium or might be involved in the transport of selenium. May supply selenium to tissues such as brain and testis.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: Made in the liver and heart and secreted into the plasma. It is also found in the kidney.			
CC	-!- MISCELLANEOUS: The selenocysteines are all encoded by the opal			

```

CC -----
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CC -----
DR EMBL; Z11793; CAA77836.1; --
DR PIR; A47327; A47327.
DR Genew; HGNC:10751; SEPP1.
DR MIM; 601484; --
DR GO; GO:0008430; F:selenium binding; TAS.
DR GO; GO:0006979; P:response to oxidative stress; TAS.
DR InterPro; IPR007672; Selp_C.
DR Pfam; PF04593; Selp_C; 1.
DR InterPro; IPR007671; Selp_N.
DR Pfam; PF04592; Selp_N; 1.
DR Direct protein sequencing; Glycoprotein; Plasma; Selenium;
KW Selenocysteine; Signal.
FT SIGNAL 1 19
FT CHAIN 20 381 Selenoprotein P.
FT DOMAIN 244 249 Poly-His.
FT SE_CYS 59 59
FT SE_CYS 300 300
FT SE_CYS 318 318
FT SE_CYS 330 330
FT SE_CYS 345 345
FT SE_CYS 352 352
FT SE_CYS 367 367
FT SE_CYS 369 369
FT SE_CYS 376 376
FT SE_CYS 378 378
FT CARBOHYD 46 46 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 83 83 N-linked (GlcNAc... ) (By similarity).
FT CARBOHYD 119 119 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 128 128 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 174 174 N-linked (GlcNAc... ) (By similarity).
FT CARBOHYD 338 338 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 381 AA; 42705 MW; 1A82FFA0BCD13CD7 CRC64;

Query Match 94.7%; Score 479; DB 1; Length 381;
Best Local Similarity 91.3%; Pred. No. 1.5e-45;
Matches 94; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KRCINQLLCKLPDSELPAPRSCCHRLIFPKTGSALTCKENLPSLCSXQGLRAEN 60
Db 279 KRCINQLLCKLPDSELPAPRSCCHRLIFPKTGSALTCKENLPSLCSXQGLRAEN 338

Qy 61 ITESCOXRLPPAAQISQQLIPTASASXRNQKQAKKXCPN 103
Db 339 ITESCOXRLPPAAQISQQLIPTASASXRNQKQAKKXCPN 381

RESULT 2
Q6PD59 PRELIMINARY; PRT; 381 AA.
AC Q6PD59;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Selenoprotein P..
CN Name=SEPP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow, and Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

```

```

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC058919; AAH58919.1; -.
DR EMBL; BC005244; AAH05244.1; -.
DR GO; GO:0008430; F:selenium binding; IEA.
DR InterPro; IPR007672; Selp_C.
DR InterPro; IPR007671; Selp_N.
DR Pfam; PF04593; Selp_C; 1.
DR Pfam; PF04592; Selp_N; 1.
DR Selenium; Selenocysteine.
FT SE_CYS 59 59
FT SE_CYS 300 300
FT SE_CYS 318 318
FT SE_CYS 330 330
FT SE_CYS 345 345
FT SE_CYS 352 352
FT SE_CYS 367 367
FT SE_CYS 369 369
FT SE_CYS 376 376
FT SE_CYS 378 378
SQ SEQUENCE 381 AA; 42734 MW; 7A00BE7762D90833 CRC64;

Query Match 94.7%; Score 479; DB 2; Length 381;
Best Local Similarity 91.3%; Pred. No. 1.5e-45;
Matches 94; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KRCINQLLCKLPDSELPAPRSCCHRLIFPKTGSALTCKENLPSLCSXQGLRAEN 60
Db 279 KRCINQLLCKLPDSELPAPRSCCHRLIFPKTGSALTCKENLPSLCSXQGLRAEN 338

Qy 61 ITESCOXRLPPAAQISQQLIPTASASXRNQKQAKKXCPN 103
Db 339 ITESCOXRLPPAAQISQQLIPTASASXRNQKQAKKXCPN 381

RESULT 3
Q6PI87 PRELIMINARY; PRT; 381 AA.
ID Q6PI87
AC Q6PI87;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Selenoprotein P..
CN Name=SEPP1;
OS Homo sapiens (Human).

```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC040075; AAH40075.1; -;
 DR GO; GO:0008430; F:selenium binding; IEA.
 DR InterPro; IPR007672; Selp_C.
 DR InterPro; IPR007671; Selp_N.
 DR Pfam; PF04593; Selp_C; 1.
 DR Pfam; PF04592; Selp_N; 1.
 KW Selenium; Selenocysteine.
 FT SE_CYS 300 300
 FT SE_CYS 318 318
 FT SE_CYS 330 330
 FT SE_CYS 345 345
 FT SE_CYS 352 352
 FT SE_CYS 367 367
 FT SE_CYS 369 369
 FT SE_CYS 376 376
 FT SE_CYS 378 378
 FT SE_CYS 59 59
 SQ SEQUENCE 381 AA; 42704 MW; 7A14EF3D32370983 CRC64;
 Query Match 94.7%; Score 479; DB 2; Length 381;
 Best Local Similarity 91.3%; Pred. No. 1.5e-45;
 Matches 94; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 KRCINQLCKLPDSELA PRSCCHRLIFPKTGSAITXQCKENLPSCSQGLRAEN 60
 Db 279 KRCINQLCKLPDSELA PRSCCHRLIFPKTGSAITXQCKENLPSCSQGLRAEN 338
 QY 61 ITESCQXRLPPAAXQISOQLIPTASASXRXKXQAKKXEPSN 103
 Db 339 ITESCQXRLPPAAXQISOQLIPTASASXRXKXQAKKXEPSN 381
 RESULT 4
 Q6PJF9 PRELIMINARY; PRT; 381 AA.
 AC Q6PJF9;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Selenoprotein P,
 GN Name=SRPPI;

OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
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 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015875; AAH15875.1; -;
 DR GO; GO:0008430; F:selenium binding; IEA.
 DR InterPro; IPR007672; Selp_C.
 DR InterPro; IPR007671; Selp_N.
 DR Pfam; PF04593; Selp_C; 1.
 DR Pfam; PF04592; Selp_N; 1.
 KW Selenium; Selenocysteine.
 FT SE_CYS 300 300
 FT SE_CYS 318 318
 FT SE_CYS 330 330
 FT SE_CYS 345 345
 FT SE_CYS 352 352
 FT SE_CYS 367 367
 FT SE_CYS 369 369
 FT SE_CYS 376 376
 FT SE_CYS 378 378
 FT SE_CYS 59 59
 SQ SEQUENCE 381 AA; 42705 MW; 4C195CA317ACBA1D CRC64;
 Query Match 94.7%; Score 479; DB 2; Length 381;
 Best Local Similarity 91.3%; Pred. No. 1.5e-45;
 Matches 94; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 KRCINQLCKLPDSELA PRSCCHRLIFPKTGSAITXQCKENLPSCSQGLRAEN 60
 Db 279 KRCINQLCKLPDSELA PRSCCHRLIFPKTGSAITXQCKENLPSCSQGLRAEN 338
 QY 61 ITESCQXRLPPAAXQISOQLIPTASASXRXKXQAKKXEPSN 103
 Db 339 ITESCQXRLPPAAXQISOQLIPTASASXRXKXQAKKXEPSN 381
 RESULT 5
 Q6PI43 PRELIMINARY; PRT; 381 AA.
 ID Q6PI43;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Selenoprotein P,

DE	Selenoprotein P.
DGN	Name=Self;
OS	Bos taurus (Bovine).
KOC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OCC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OCC	Bovinae; Bos.
OX	NCBI_TaxID=9913;
[1]	
RN	SEQUENCE FROM N.A.
RP	Hara S., Imura N., Shoji Y.;
RA	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RRL	EMBL; AB032826; BAA84781.1; -
DR	GO: GO:0008430; F:selenium binding; IEA.
DR	InterPro; IPR007672; Selp_C.
DR	InterPro; IPR007671; Selp_N.
DR	Pfam; PF04593; Selp_C; 1.
DR	Pfam; PF04592; Selp_N; 1.
DR	Selenium; Selenocysteine.
FT	SE_CYS 281 281
FT	SE_CYS 291 291
FT	SE_CYS 322 322
FT	SE_CYS 334 334
FT	SE_CYS 347 347
FT	SE_CYS 349 349
FT	SE_CYS 356 356
FT	SE_CYS 372 372
FT	SE_CYS 374 374
FT	SE_CYS 381 381
FT	SE_CYS 383 383
FT	SE_CYS 59 59
FS	SEQUENCE 386 AA; EC6F3A76874E528F CRC64;
QY	Query Match 71.6%; Score 362.5; DB 2; Length 386;
DB	Best Local Similarity 70.2%; Pred. No. 2e-32;
QY	Matches 73; Conservative 6; Mismatches 24; Indels 1; Gaps 1;
DB	1 KRCINOLLCKLPDSELAPRSXCHCHHLIFETGSAITXCKENLPSCSXQGLRAEN 60 283 KRCINOLLCPFKDSALSSCCHHVLFEKTSAITXCCTEKPLSLCSQGLLAEN 342
QY	61 ITESCOKRLLPAAAXQIS-QQLIPTESASXXRXKNQAQKCEPSN 103
DB	343 VIESQCCELPPAACQAAGQQLNPTASTKCSCKNAKWCKCFSN 386
RESULT 7	
ID	_SELF_BOVIN STANDARD; PRT; 402 AA.
AC	P49907; O193003;
DT	01-OCT-1996 (Rel. 34, Created)
DD	01-OCT-1996 (Rel. 34, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Selenoprotein P-like protein precursor.
DN	Name=SEPP1; Synonyms=SELP;
OS	Bos taurus (Bovine).
OCC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OCC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OCC	Bovinae; Bos.
OX	NCBI_TaxID=9913;
[1]	
RP	SEQUENCE FROM N.A.
RC	TSSUE=Cerbellum;
EX	MEDLINE=95364621; PubMed=7637580; DOI=10.1016/0169-328X(94)00007-2;
RA	Sajion K., Saito N., Lee M.J., Fujii M., Kobayashi T., Sumino K.;
RT	"Molecular cloning of cDNA encoding a bovine selenoprotein P-like
RT	protein containing 12 selenocysteines and a (His-Pro) rich domain
RT	insertion, and its regional expression.";
RL	Brain Res. Mol. Brain Res. 30:301-311(1995). [2]
RP	SEQUENCE FROM N.A.
EX	MEDLINE=98019090; PubMed=9358058; DOI=10.1016/S0378-1119(97)00369-7;
RA	Fujii M., Sajion K., Kobayashi T., Fujii S., Lee M.J., Sumino K.;
RT	"Analysis of bovine selenoprotein P-like protein gene and availability


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FT CONFLICT 188 188 T -> N (in Ref. 2).
FT CONFLICT 192 192 A -> V (in Ref. 2).
FT CONFLICT 203 203 A -> V (in Ref. 2).
SQ SEQUENCE 380 AA; 42236 MW; 72F7031941F47212 CRC64;

Query Match 63.7%; Score 322.5; DB 1; Length 380;
Best Local Similarity 64.4%; Pred. No. 6.2e-28;
Matches 65; Conservative 9; Mismatches 26; Indels 1; Gaps 1;

Qy 3 CINOLLCKLPDSELPASRSCCHCHLIFKTSNAITXQCKENLPSCSXGLRAENIT 62
Db 281 CINOLLCKLSKESAAPSSCCCHCHLIFKTSNAITXQCKENLPSCSXGLRAENIT 340

Qy 63 ESCOXRLPPAAQXISQOLIPTEASASXXKXNQAKKXEPSN 103
Db 341 ESCQCRSPPAACQ-NQPNPMEANPNCSCDQTKCKCHSN 380

RESULT 9
ID Q80T08 PRELIMINARY; PRT; 380 AA.
AC Q80T08;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
DE RIKEN full-length enriched library, clone:5031434C21
DE product:selenoprotein P, plasma, 1, full insert sequence.
GN Name=Seppli;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima J., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK077265; BAC55264.2; -.
DR MGD; MGI-894288; Seppli.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008430; F:selenium binding; IDA.
DR GO; GO:0007420; P:brain development; IMP.
DR GO; GO:0040007; P:growth; IMP.
DR GO; GO:0007626; P:locomotory behavior; IMP.
DR GO; GO:0009791; P:post-embryonic development; IMP.
DR GO; GO:0001887; P:selenium metabolism; IDA.
DR GO; GO:0019953; P:sexual reproduction; IMP.
DR InterPro; IPR007672; Selp_C.
DR InterPro; IPR007671; Selp_N.
DR Pfam; PF04593; Selp_C; 1.
DR Pfam; PF04592; Selp_N; 1.
DR Selenium; Selenocysteine.
KW SE_CYS 259 259
FT SE_CYS 277 277
FT SE_CYS 318 318
FT SE_CYS 330 330
FT SE_CYS 352 352
FT SE_CYS 366 366
FT SE_CYS 368 368
FT SE_CYS 372 372
FT SE_CYS 375 375
FT SE_CYS 377 377
FT SE_CYS 59 59
SQ SEQUENCE 380 AA; 42272 MW; 4D1EB91BD89F89D1 CRC64;

Query Match 63.5%; Score 321.5; DB 2; Length 380;
Best Local Similarity 63.4%; Pred. No. 8e-28;
Matches 64; Conservative 10; Mismatches 26; Indels 1; Gaps 1;

Qy 3 CINOLLCKLPDSELPASRSCCHCHLIFKTSNAITXQCKENLPSCSXGLRAENIT 62
Db 281 CINOLLCKLSKESAAPSSCCCHCHLIFKTSNAITXQCKENLPSCSXGLRAENIT 340

Qy 63 ESCOXRLPPAAQXISQOLIPTEASASXXKXNQAKKXEPSN 103
Db 341 ESCQCRSPPAACQ-NQPNPMEANPNCSCDQTKCKCHSN 380

RESULT 10
ID Q80UF3 PRELIMINARY; PRT; 380 AA.
AC Q80UF3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male kidney cDNA, RIKEN full-length enriched
DE library, clone:0610010C08 product:selenoprotein P, plasma, 1, full
DE insert sequence.
GN Name=Seppli;
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RL "High-efficiency full-length cDNA cloning.";
 RN Meth. Enzymol. 303:19-44(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RL "Functional annotation of a full-length mouse cDNA collection.";
 RN Nature 409:685-690(2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RA The FANTOM Consortium;
 RL "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RN Nature 420:563-573(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RL "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 RN Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaibiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RL "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 RN Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saïto H., Saïto R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK002450; BAC55246.2; -;
 DR MGI; 894288; Seppl.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0008430; F:selenium binding; IDA.
 DR GO; GO:0007420; P:brain development; IMP.
 DR GO; GO:0040007; P:growth; IMP.
 DR GO; GO:0007626; P:locomotory behavior; IMP.
 DR GO; GO:0009791; P:post-embryonic development; IMP.
 DR GO; GO:0001887; P:selenium metabolism; IDA.
 DR GO; GO:0019953; P:sexual reproduction; IMP.

DR InterPro; IPR007672; Selp_C.
 DR InterPro; IPR007671; Selp_N.
 DR Pfam; PF04593; Selp_C; 1.
 DR Pfam; PF04592; Selp_N; 1.
 KW Selenium; Selenocysteine.
 FT SE_CYS 259 259
 FT SE_CYS 277 277
 FT SE_CYS 318 318
 FT SE_CYS 321 321
 FT SE_CYS 330 330
 FT SE_CYS 352 352
 FT SE_CYS 366 366
 FT SE_CYS 368 368
 FT SE_CYS 375 375
 FT SE_CYS 377 377
 FT SE_CYS 59 59
 SQ SEQUENCE 380 AA; 42268 MW; 72F7031B43F47010 CRC64;
 Query Match 63.3%; Score 320.5; DB 2; Length 380;
 Best Local Similarity 64.4%; Pred. No. le-27; Indels 1; Gaps 1;
 Matches 65; Conservative 9; Mismatches 26;
 OY 3 CINOLLCKLPDSELAPRSXCHCHRLIFETKTSAITXQCKENLPSLCSXQGLRAENIT 62
 DB 281 CINOLLCKLSKESAEAPSSCCCHCHRLIFKSGSAIACCCENLPSLSCQGLFAEEKVT 340
 OY 63 ESCQXRLPPAAQISQQLIPTEASAXXKXQAKKEXPSN 103
 DB 341 ESCQCRSPPAACQ-NQPMNPMNPNCSNCDNTRKCKCHSN 380
 RESULT 11
 Q6PK67
 ID Q6PK67 PRELIMINARY; PRT; 380 AA.
 AC Q6PK67;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Selenoprotein P, plasma, 1.
 GN Name=Seppl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RL "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

EMBL; BC001991; AAH01991.2; --
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0008430; F:selenium binding; IDA.
 DR GO; GO:0007420; P:brain development; IMP.
 DR GO; GO:0040007; P:growth; IMP.
 DR GO; GO:0007626; P:locomotory behavior; IMP.
 DR GO; GO:0009791; P:post-embryonic development; IMP.
 DR GO; GO:0001887; P:selenium metabolism; IDA.
 DR GO; GO:0019953; P:sexual reproduction; IMP.
 DR InterPro; IPR007672; Selp_C.
 DR InterPro; IPR007671; Selp_N.
 DR Pfam; PF04593; Selp_C; 1.
 DR Pfam; PF04592; Selp_N; 1.
 DR Selenium; Selenocysteine.
 KW SE_CYS 259 259
 FT SE_CYS 277 277
 FT SE_CYS 318 318
 FT SE_CYS 321 321
 FT SE_CYS 330 330
 FT SE_CYS 352 352
 FT SE_CYS 366 366
 FT SE_CYS 368 368
 FT SE_CYS 375 375
 FT SE_CYS 377 377
 FT SE_CYS 59 59
 SQ SEQUENCE 380 AA; 42281 MW; F9FOEA15B8F39005 CRC64;
 Query Match 63.3%; Score 320.5; DB 2; Length 380;
 Best Local Similarity 64.4%; Pred. NO. 1e-27;
 Matches 65; Conservative 9; Mismatches 26; Indels 1; Gaps 1;
 QY 3 CINQLLCKLPTDSELAPRSKCHCHHLIFETKGSATITXCKENLPSCSXGLRAENIT 62
 DB 281 CINQLLCKLSESAAPSSCCCHHLIFEXSGSAIACCCENLPSCSCQGLFAEKVT 340
 QY 63 ESCQRLPPAAQIQIISQILPTASASXRXKQAKKXEPSN 103
 DB 341 ESCQCRSPAAQCNQPNPMEANFNCSNCDNTRCKCKCHSN 380
 RESULT 12
 Selp_RAT
 ID Selp_RAT STANDARD; PRT; 385 AA.
 AC P25236;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Selenoprotein P precursor (Sep).
 GN Name=Seppl; Synonyms=Selp;
 OS Rattus norvegicus (Rat)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-41; 267-287 AND 316-327.
 RC TISSUE=Liver;
 RX MEDLINE=91244760; PubMed=2037562;
 RA Hill K.E., Lloyd R.S., Yang J.-G., Read R., Burk R.F.;
 RT "The cDNA for rat selenoprotein P contains 10 TGA codons in the open
 reading frame."
 RL J. Biol. Chem. 266:10050-10053 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Kidney;
 RX MEDLINE=95364621; PubMed=7637580; DOI=10.1016/0169-328X(94)00007-2;
 RA Saijoh K., Saito N., Lee M.J., Kobayashi T., Sumino K.;
 RT "Molecular cloning of cDNA encoding a bovine selenoprotein P-like
 protein containing 12 selenocysteines and a (His-Pro) rich domain
 insertion, and its regional expression."
 RL Brain Res. Mol. Brain Res. 30:301-311 (1995).
 RN [3]
 RP CHARACTERIZATION OF ISOFORMS.
 RX PubMed=11821412; DOI=10.1074/jbc.M111462200;

RA Ma S., Hill K.E., Caprioli R.M., Burk R.F.;
 RT "Mass spectrometric characterization of full-length rat selenoprotein
 P and three isoforms shortened at the C terminus. Evidence that three
 UGA codons in the mRNA open reading frame have alternative functions
 of specifying selenocysteine insertion or translation termination.";
 RL J. Biol. Chem. 277:12749-12754 (2002).
 RN [4]
 RP CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX PubMed=12911312; DOI=10.1021/bi0346300;
 RA Ma S., Hill K.E., Burk R.F., Caprioli R.M.;
 RT "Mass spectrometric identification of N- and O-glycosylation sites of
 full-length rat selenoprotein P and determination of selenide-sulfide
 and disulfide linkages in the shortest isoform.";
 RL Biochemistry 42:9703-9711 (2003).
 RN [5]
 RP REVIEW
 RX MEDLINE=95017128; PubMed=7931697;
 RA Burk R.F., Hill K.E.;
 RT "Selenoprotein P. A selenium-rich extracellular glycoprotein.";
 RL J. Nutr. 124:1891-1897 (1994).
 CC -!- FUNCTION: Might be responsible for some of the extracellular
 antioxidant defense properties of selenium or might be involved in
 the transport of selenium. May supply selenium to tissues such as
 brain and testis.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Widely expressed, mainly by the liver.
 CC Secreted in plasma.
 CC -!- PTM: Isoform Se-P1 contains several disulfide bridges and a
 selenide-sulfide bond between Sec-59 and Cys-62. These bonds are
 speculated to serve as redox active pairs.
 CC -!- MISCELLANEOUS: Plasma contains 4 isoforms, which are named
 isoforms Se-P10, Se-P6, Se-P2 and Se-P1, according to the number
 of selenocysteines they contain. All isoforms arise from the same
 mRNA. The 3 shortened isoforms terminated at the opal STOP codons
 at positions 264, 282, 371, when selenocysteine has not been
 inserted.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M63574; AAA42129.2; --
 CC EMBL; D25221; BAA04950.2; --
 CC PIR; A40380; OMRTSP.
 CC RGD; 3660; Seppl.
 CC InterPro; IPR007672; Selp_C.
 CC InterPro; IPR007671; Selp_N.
 CC Pfam; PF04593; Selp_C; 1.
 CC Pfam; PF04592; Selp_N; 1.
 KW Direct protein sequencing; Glycoprotein; Plasma; Selenium;
 KW Selenocysteine; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 263 Selenoprotein P, isoform Se-P1.
 FT CHAIN 20 281 Selenoprotein P, isoform Se-P2.
 FT CHAIN 20 370 Selenoprotein P, isoform Se-P6.
 FT CHAIN 20 385 Selenoprotein P, isoform Se-P10.
 FT DOMAIN 244 252 Poly-His.
 FT CROSSLINK 59 62 CysteinyI-selenocysteine (Sec-Cys) (in
 isoform Se-P1).
 FT FT In isoform Se-P1.
 FT FT In isoform Se-P1.
 FT DISULFID 168 186
 FT DISULFID 172 175
 FT SE_CYS 59 59
 FT SE_CYS 264 264
 FT SE_CYS 282 282
 FT SE_CYS 323 323
 FT SE_CYS 335 335
 FT SE_CYS 357 357
 FT SE_CYS 371 371
 FT SE_CYS 373 373

```

FT SE_CYS 380 382
FT SE_CYS 382 382
FT CARBOHYD 83 83 N-linked (GlcNAc...)
FT CARBOHYD 174 174 N-linked (GlcNAc...)
FT CARBOHYD 188 188 N-linked (GlcNAc...)
FT CARBOHYD 365 365 O-linked (Hex...); partial.
SQ SEQUENCE 385 AA; 42614 MW; 42614 MW; 013BDF4FB741E3E8 CRC64;

Query Match 61.2%; Score 309.5; DB 1; Length 385;
Best Local Similarity 66.3%; Pred. No. 1.8e-26;
Matches 63; Conservative 6; Mismatches 25; Indels 1; Gaps 1;

QY 3 CINOLLCKLPDSELPASXCHCHRLIFKTSQSAITX--QCKENLPSLSCXQGLRAENIT 62
Db 286 CINOLLCKLSESGAATSSCCHCHRLIFKTSQSAITX--QCKENLPSLSCXQGLRAENIT 62
QY 63 ESCQXRLPPAAKQISQQLIPTASASXRXKXQAKK 97
Db 346 ESCQXRLPPAAKQISQQLIPTASASXRXKXQAKK 97
Db 346 ESCQXRLPPAAKQISQQLIPTASASXRXKXQAKK 97

RESULT 13
ID SEPA BRARE STANDARD; PRT; 367 AA.
AC Q985V1.
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DB Selenoprotein Pa precursor (zSelpa).
GN Name=selpa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=2110713; PubMed=11168591;
RA Kryukov G.V., Gladyshev V.N.;
RT "Selenium metabolism in zebrafish: multiplicity of selenoprotein genes
RL and expression of a protein containing 17 selenocysteine residues.";
RL Genes Cells 5:1049-1060(2000).
CC -!- FUNCTION: Might be responsible for some of the extracellular
CC antioxidant defense properties of selenium or might be involved in
CC the transport of selenium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: The selenocysteines are all encoded by the opal
CC codon, UGA.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF322071; AAG53688.1; -.
CC ZFIN; ZDB-GENE-030311-1; selpa.
CC GO; GO:0005576; C:extracellular; IDA.
CC GO; GO:0006979; P:response to oxidative stress; NAS.
CC InterPro; IPR007672; Selp_C.
CC InterPro; IPR007671; Selp_N.
CC Pfam; PF04593; Selp_C; 1.
CC Pfam; PF04592; Selp_N; 1.
CC Glycoprotein; Selenium; Selenocysteine; Signal.
KW SIGNAL
FT CHAIN 1 19 Potential.
FT CHAIN 20 367 Selenoprotein Pa.
FT DOMAIN 204 235 His-rich.
FT DOMAIN 267 364 Cys-rich.
FT SE_CYS 59 59
FT SE_CYS 267 267
FT SE_CYS 273 273

```

```

FT SE_CYS 279 279
FT SE_CYS 290 290
FT SE_CYS 292 292
FT SE_CYS 294 294
FT SE_CYS 310 310
FT SE_CYS 320 320
FT SE_CYS 322 322
FT SE_CYS 336 336
FT SE_CYS 338 338
FT SE_CYS 346 346
FT SE_CYS 353 353
FT SE_CYS 355 355
FT SE_CYS 362 362
FT SE_CYS 364 364
FT CARBOHYD 109 109
SQ SEQUENCE 367 AA; 41170 MW; 53710716A57FCE5B CRC64;

Query Match 26.8%; Score 135.5; DB 1; Length 367;
Best Local Similarity 37.6%; Pred. No. 6.5e-07;
Matches 38; Conservative 13; Mismatches 35; Indels 15; Gaps 6;

QY 2 RCINOLLCKLPDSELPASXCHCHRLIFKTSQSAITX--QCKENLPSLSCXQGLRAEB 59
Db 272 RCKVQSCQAGADSPVA--SCCCHCRLFGGEGNVRVAGLCHCDEPLPASCPCQGLKEQD 329
QY 60 N-ITESCOXR-LPPAAKQISQQLIPT-----EASASRXK 92
Db 330 NHKETCQCPAPPAPAECELSQ---PTVCVPAGDATCGCRKK 367

RESULT 14
Q6P3K0 PRELIMINARY; PRT; 367 AA.
ID Q6P3K0.
AC Q6P3K0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Seppia protein.
GN Name=seppia;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC063960; AAHG3960.1; -.
DR ZFIN; ZDB-GENE-030311-1; seppia.
DR GO; GO:0008430; F:selenium binding; IEA.
DR InterPro; IPR007672; Selp_C.
DR InterPro; IPR007671; Selp_N.
DR Pfam; PF04593; Selp_C; 1.
DR Pfam; PF04592; Selp_N; 1.
DR Selenium; Selenocysteine.
FT SE_CYS 267 267
FT SE_CYS 273 273
FT SE_CYS 279 279
FT SE_CYS 290 290
FT SE_CYS 292 292
FT SE_CYS 294 294
FT SE_CYS 310 310
FT SE_CYS 320 320
FT SE_CYS 322 322
FT SE_CYS 336 336
FT SE_CYS 338 338
FT SE_CYS 346 346
FT SE_CYS 353 353
FT SE_CYS 355 355
FT SE_CYS 362 362
FT SE_CYS 364 364
FT SE_CYS 59 59
SQ SEQUENCE 367 AA; 41142 MW; BEC7DC62373CTF73 CRC64;

Query Match      26.8%; Score 135.5; DB 2; Length 367;
Best Local Similarity 37.6%; Pred. No. 6.5e-07;
Matches 38; Conservative 13; Mismatches 35; Indels 15; Gaps 6;

QY 2 RCINQLLCKLPDSELPSCCHCHLIFKGTGSAITX--QCKENLPSCSXQGLRAEE 59
DB 272 RCKVQYSCQGGADSPVA--SCCHCRQLFGGNGRVRAGLCHCDPLPASCPCQQLKEQD 329

QY 60 N-ITBSCQXR-LPPAAXQISQOLIPT-----EASASXRXK 92
DB 330 NHIKETCQCRAPPAPCELSQ---PTCVCPAGDAGTCGCKK 367

RESULT 15
PCLO HUMAN
ID PCLO_HUMAN STANDARD; PRT; 5183 AA.
AC Q9Y6V0; O43373; O60305; Q9BVC8; Q9UIV2; Q9Y6U9;
DI 28-FEB-2003 (Rel. 41, Created)
DT 29-WAR-2004 (Rel. 43, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Piccolo protein (Aczonin).
GN Name=PCLO; Synonyms=ACZ, KIAA0559;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
EX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Meas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fellw G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du P., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Stromatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,

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Baertsch R.A., Brent M.R., Keibler E., Fliceck P., Bork P., Suyama M., Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R., Bady S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D., Waterston R.H., Wilson R.K.; "The DNA sequence of human chromosome 7."; Nature 424:157-164 (2003).

[2] SEQUENCE OF 37-795 FROM N.A. (ISOFORMS 1/2).
TISSUE=Brain;
MEDLINE=9439764; PubMed=1050862; DOI=10.1083/jcb.147.1.151;
Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E., Kilmann M.W.; "Aczonin, a 550-kd putative scaffolding protein of presynaptic active zones, shares homology regions with rim and bassoon and binds profilin."; J. Cell Biol. 147:151-162 (1999).

[3] SEQUENCE OF 3655-5183 FROM N.A. (ISOFORM 2).
TISSUE=Brain;
MEDLINE=98290545; PubMed=9628581;
Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 5:31-39 (1998).

[4] SEQUENCE OF 4440-4473 FROM N.A. (ISOFORM 2).
TISSUE=Placenta;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: May act as a scaffolding protein involved in the organization of synaptic active zones and in synaptic vesicle trafficking (By similarity).

-!- SUBUNIT: Interacts with Rabac1/Pral, RIMS2 and profilin (By similarity).

-!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of synaptic junctions (By similarity).

-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=1;
IsoId=Q9Y6V0-1; Sequence=Displayed;
Name=2;
IsoId=Q9Y6V0-2; Sequence=VSP_003923, VSP_003924, VSP_003925, VSP_003926, VSP_003927;

-!- DOMAIN: C2 domain 1 is involved in binding calcium and phospholipids. Calcium binds with low affinity but with high specificity and induces a large conformational change.

-!- SIMILARITY: Contains 2 C2 domains.

-!- SIMILARITY: Contains 1 PDZ/DHR domain.

-!- CAUTION: Ref.1 (A021789) sequence differs from that shown due to erroneous gene model prediction.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2005, 09:30:34 ; Search time: 172 Seconds
(without alignments)
231.607 Million cell updates/sec

Title: US-09-856-199-3

Perfect score: 506

Sequence: 1 KRCINQLLCKLPTDSELA...BASASXXKXKQAKXKXPSN 103

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	96.4	103	6	ABP71716 Human sel
2	488	96.4	103	6	ABP55510 Human pla
3	488	96.4	103	6	ABP57372 Selenopro
4	488	96.4	103	6	ABP59457 Amino aci
5	488	96.4	103	7	ADP53279 Human sel
6	488	96.4	103	8	ADO71758 Human sel
7	488	96.4	103	8	ADP90528 C-termina
8	488	96.4	362	8	ADO71757 Human sel
9	488	96.4	362	8	ADP90527 Human sel
10	488	96.4	381	5	AAU84306 Human end
11	488	96.4	381	6	ABU89753 Protein d
12	488	96.4	381	7	ADP65180 Human sel
13	482	95.3	380	7	ADN95151 Human BEC
14	479	94.7	103	3	ABP57373 Selenopro
15	479	94.7	381	3	ABP59458 Amino aci
16	479	94.7	381	7	ADP53279 Human sel
17	309.5	61.2	385	7	ADD47224 Rat Prote
18	182	36.0	33	6	ABP55511 Human pla
19	182	36.0	33	6	ABP57373 Selenopro
20	182	36.0	33	6	ABP59458 Amino aci
21	182	36.0	33	8	ADO71759 Human sel
22	182	36.0	33	8	ADP90529 Human sel
23	166	32.8	30	7	ADF53280 Human sel
24	162	32.0	29	5	AAU97702 Human sel
25	162	32.0	29	6	ABP55508 Human pla

ALIGNMENTS

RESULT 1

ABP71716

ID ABP71716 standard; peptide; 103 AA.

AC ABP71716;

DT 17-APR-2003 (first entry)

DE Human selenoprotein P C-terminal peptide fragment # SEQ ID 3.

KW Neurodegenerative disease; selenoprotein P; neurotropic; neuroprotective; anticonvulsant; motor ataxia; Alzheimer's disease; senile dementia; Huntington's chorea; supranuclear paralysis; epilepsy; human; spinocerebellar degeneration.

OS Homo sapiens.

XX Key Location/Qualifiers

FH Modified-site 22

FT /label= OTHER

FT /note= "selenocysteine"

FT Modified-site 40

FT /label= OTHER

FT /note= "selenocysteine"

FT Modified-site 52

FT /label= OTHER

FT /note= "selenocysteine"

FT Modified-site 67

FT /label= OTHER

FT /note= "selenocysteine"

FT Modified-site 74

FT /label= OTHER

FT /note= "selenocysteine"

FT Modified-site 89

FT /label= OTHER

FT /note= "selenocysteine"

FT Modified-site 91

FT /label= OTHER

FT /note= "selenocysteine"

FT Modified-site 100

FT /label= OTHER

FT /note= "selenocysteine"

PN WO200292121-A1.

XX 21-NOV-2002.

PD 10-MAY-2002; 2002WO-JP004558.

XX 10-MAY-2002; 2002WO-JP004558.

PF 10-MAY-2002; 2002WO-JP004558.

26	162	32.0	29	6	ABB99455	Abb999455	Amino aci
27	162	32.0	29	8	ADO71760	Ado71760	Human sel
28	162	32.0	29	8	ADP90530	Adp90530	Human sel
29	161	31.8	29	3	AA03183	Aa03183	Human sel
30	132	26.1	28	5	AAU97703	Aau97703	Human sel
31	132	26.1	28	6	ABP55509	Abp55509	Human pla
32	132	26.1	28	6	ABB99456	Abb99456	Amino aci
33	132	26.1	28	7	ADF53281	Adf53281	Human sel
34	132	26.1	28	8	ADO71761	Ado71761	Human sel
35	132	26.1	28	8	ADP90531	Adp90531	Human sel
36	130	25.7	28	3	AA03184	Aa03184	Human sel
37	111	21.9	21	3	AA03187	Aa03187	Human sel
38	111	21.9	21	6	ABP71718	Abp71718	Human neu
39	111	21.9	21	6	ABP55512	Abp55512	Human pla
40	111	21.9	21	6	ABP57374	Abp57374	Selenopro
41	111	21.9	21	6	ABB99459	Abb99459	Amino aci
42	111	21.9	110	3	AA03755	Aa03755	Human sec
43	111	21.9	240	3	AA057080	Aa057080	Human pro
44	111	21.9	299	7	AD040114	Ad040114	Human nov
45	107	21.1	20	3	AA03186	Aa03186	Human sel

```

XX 11-MAY-2001; 2001JP-00141462.
XX
XX (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX (HISM ) HISAMITSU PHARM CO LTD.
XX
XX Hirashina M, Naruse T, Maeda H, Nozaki C, Goto T, Akiyama K;
XX PI Fukushima H;
XX
XX WPI; 2003-156710/15.
XX
XX New remedies for neurodegenerative diseases showing motor ataxia as major
XX PT symptom such as Alzheimer's disease, senile dementia, Huntington's chorea
XX PT and supranuclear paralysis, comprising selenoprotein P or its C-terminal
XX PT peptide(s).
XX
XX Example 2; Page 9; 31pp; Japanese.
XX
XX The invention relates to new remedies for neurodegenerative diseases
XX CC comprising selenoprotein P, or its C-terminal peptide(s). The activity of
XX CC peptides of the invention may be described as nootropic, neuroprotective
XX CC and anticonvulsant. The remedies are for neurodegenerative diseases
XX CC showing motor ataxia as a major symptom. These include (juvenile)
XX CC Alzheimer's disease, senile dementia, Huntington's chorea, supranuclear
XX CC paralysis, spinocerebellar degeneration and difficult-to-cure epilepsy.
XX CC The current sequence represents the human selenoprotein P C-terminal
XX CC peptide fragment
XX
XX Sequence 103 AA;
XX
XX Query Match 96.4%; Score 488; DB 6; Length 103;
XX Best Local Similarity 100.0%; Pred.No. 6;7e-50;
XX Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX QY 1 KRCINOLLCKLPDSELAPRSCXCHRLIFEKTSAITXQCKENLPSLCSXQGLFAEEN 60
XX DB 1 KRCINOLLCKLPDSELAPRSCXCHRLIFEKTSAITXQCKENLPSLCSXQGLFAEEN 60
XX
XX QY 61 ITESCQXRLPPAAXQISQOLIPTASASRXKXKQAKKXEPSN 103
XX DB 61 ITESCQXRLPPAAXQISQOLIPTASASRXKXKQAKKXEPSN 103
XX
XX RESULT 2
XX ABP55510
XX ID ABP55510 standard; protein; 103 AA.
XX
XX AC ABP55510;
XX
XX DT 18-FEB-2003 (first entry)
XX
XX Human plasma selenoprotein P SEQ ID NO:3.
XX
XX Human; plasma; selenoprotein P; neurodegenerative disease;
XX KW motor disorder; depression; nootropic; neuroprotective; anticonvulsant;
XX KW cerebroprotective; aging; traumatic cerebrovascular damage; epilepsy;
XX KW motorneuron disease.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 22 /note= "selenocysteine"
XX FT Modified-site 40 /note= "selenocysteine"
XX FT Modified-site 52 /note= "selenocysteine"
XX FT Modified-site 67 /note= "selenocysteine"
XX FT Modified-site 74 /note= "selenocysteine"
XX FT Modified-site 89 /note= "selenocysteine"
XX FT Modified-site /note= "selenocysteine"

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FT Modified-site /note= "selenocysteine"
 FT 52 /note= "selenocysteine"
 FT 67 /note= "selenocysteine"
 FT 74 /note= "selenocysteine"
 FT 89 /note= "selenocysteine"
 FT 91 /note= "selenocysteine"
 FT 98 /note= "selenocysteine"
 FT 100 /note= "selenocysteine"
 FT 100 /note= "selenocysteine"
 XX
 PN WO200292810-A1.
 XX
 XX 21-NOV-2002.
 XX
 PF 10-MAY-2002; 2002WO-JP004557.
 XX
 PR 11-MAY-2001; 2001JP-00141466.
 XX
 PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX
 PI Hirashima M, Naruse T, Maeda H, Nozaki C, Goto T, Akiyama K;
 PI Hattori W;
 XX
 DR WPI; 2003-129291/12.
 XX
 XX Screening of functional peptides with lower cytotoxicity than
 PT selenocysteine and cytotoxicity inhibitory activity, for use in drugs for
 PT diseases like Alzheimer's disease, AIDS and arteriosclerosis, and in
 PT cosmetics.
 XX
 PS Example 1; Page 15; 43pp; Japanese.
 XX
 CC The present invention describes peptides (I) comprising one or more
 CC selenocysteines that show lower cytotoxicity than selenocysteine and
 CC cytotoxicity inhibitory activity. Also described is a method for
 CC screening substances with cytotoxicity inhibitory activity by using the
 CC sudden cell death phenomenon in a cell culture system with an albumin or
 CC fatty acid-added serum-free medium for culturing a test substance, and
 CC evaluating the degree of cytotoxicity based on generation of peroxidised
 CC lipid, or glutathione peroxidase activity, as indication. (I) have
 CC nootropic, neuroprotective, antiarteriosclerotic and anti-HIV activities.
 CC The screened peptides are useful for drugs for diseases like Alzheimer's
 CC disease, AIDS and arteriosclerosis, and in cosmetics. The present
 CC sequence represents a selenoprotein P fragment, which is used in an
 CC example from the present invention
 XX
 SQ Sequence 103 AA;
 Query Match 96.4%; Score 488; DB 6; Length 103;
 Best Local Similarity 100.0%; Pred. No. 6.7e-50;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPDSELAPRSXCCHRHILFEKTSALTQCKENLPSCSXQGLRABEN 60
 DB 1 KRCINQLLCKLPDSELAPRSXCCHRHILFEKTSALTQCKENLPSCSXQGLRABEN 60
 QY 61 ITESCQXRLPPAAQISOQLIPTASASRXKXNQAKKXEPSN 103
 DB 61 ITESCQXRLPPAAQISOQLIPTASASRXKXNQAKKXEPSN 103
 RESULT 4
 ABB99457
 ID ABB99457 standard; peptide; 103 AA.
 XX
 AC ABB99457;

XX 12-FEB-2003 (first entry)
 XX
 DE Amino acid sequence of a peptide derived from human selenoprotein P.
 XX
 KW Selenoprotein P; immunopathic disease; autoimmune disease;
 KW rheumatoid arthritis; multiple sclerosis; allergic disease;
 KW bronchial asthma.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 22 /note= "selenocysteine"
 FT Modified-site 40 /note= "selenocysteine"
 FT Modified-site 52 /note= "selenocysteine"
 FT Modified-site 67 /note= "selenocysteine"
 FT Modified-site 74 /note= "selenocysteine"
 FT Modified-site 89 /note= "selenocysteine"
 FT Modified-site 91 /note= "selenocysteine"
 FT Modified-site 98 /note= "selenocysteine"
 FT Modified-site 100 /note= "selenocysteine"
 FT Modified-site 100 /note= "selenocysteine"
 XX
 PN WO200276493-A1.
 XX
 XX 03-OCT-2002.
 XX
 PF 20-MAR-2002; 2002WO-JP002645.
 XX
 PR 23-MAR-2001; 2001JP-00084049.
 XX
 PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
 XX
 PI Hirashima M, Sasaki T, Naruse T, Maeda H, Nozaki C;
 XX
 DR WPI; 2003-058350/05.
 XX
 PT Selenoprotein P-derived novel drugs for preventing or treating
 PT immunopathic diseases including autoimmune diseases like rheumatoid
 PT arthritis and multiple sclerosis, and allergic diseases e.g. bronchial
 PT asthma.
 XX
 PS Disclosure; Page 7; 26pp; Japanese.
 XX
 CC The present sequence represents a C-terminal peptide of selenoprotein P.
 CC The peptide is used in drugs for preventing/treating immunopathic
 CC diseases. The drugs are used for preventing or treating immunopathic
 CC diseases including autoimmune diseases like rheumatoid arthritis and
 CC multiple sclerosis, and allergic diseases e.g. bronchial asthma
 XX
 SQ Sequence 103 AA;
 Query Match 96.4%; Score 488; DB 6; Length 103;
 Best Local Similarity 100.0%; Pred. No. 6.7e-50;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPDSELAPRSXCCHRHILFEKTSALTQCKENLPSCSXQGLRABEN 60
 DB 1 KRCINQLLCKLPDSELAPRSXCCHRHILFEKTSALTQCKENLPSCSXQGLRABEN 60
 QY 61 ITESCQXRLPPAAQISOQLIPTASASRXKXNQAKKXEPSN 103
 DB 61 ITESCQXRLPPAAQISOQLIPTASASRXKXNQAKKXEPSN 103

RESULT 5
 ID ADF53279 standard; protein; 103 AA.
 XX ADF53279;
 AC ADF53279;
 XX 12-FEB-2004 (first entry)
 DT
 XX Human selenocysteine-containing selenoprotein P.
 DE
 XX antirheumatic; antiarthritic; rheumatoid arthritis; selenocysteine;
 KW selenoprotein P.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 1..103
 FT /note= "Xaa = selenocysteine"
 FT
 XX JP2003026598-A.
 PN
 XX 29-JAN-2003.
 PD
 XX 27-JUN-2001; 2001JP-00194617.
 PF
 XX 27-JUN-2001; 2001JP-00194617.
 PR
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 PA
 XX WPI; 2003-516438/49.
 DR
 XX New rheumatoid arthritis prevention and treating agent, containing
 PT selenoprotein P and its C terminal peptide; and diagnosis of rheumatoid
 PT arthritis.
 PT
 XX Disclosure; SEQ ID NO 1; 8pp; Japanese.
 PS
 XX The invention relates to a rheumatoid arthritis (RA) prevention and
 CC treating agent comprising a selenocysteine containing protein
 CC (selenoprotein P) and/or its C terminal peptide or peptide group
 CC consisting of its partial peptide as main constituents. The C terminal
 CC peptide or peptide group consisting of a partial selenoprotein P peptide
 CC derived from amino acids 260-362. The agent containing selenoprotein P
 CC and/or C terminal peptide or its peptide family is used for the
 CC prevention or treatment of RA. It is also used for the diagnosis of
 CC immuno abnormality. This sequence corresponds to the human selenoprotein
 CC P protein from which the agents are derived.
 XX
 SQ Sequence 103 AA;
 Query Match 96.4%; Score 488; DB 7; Length 103;
 Best Local Similarity 100.0%; Pred. No. 6.7e-50;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPDSELA PRSXCHCHRLIFKETSALTQCKENLP SLCSXQGLRAEEN 60
 DB 1 KRCINQLLCKLPDSELA PRSXCHCHRLIFKETSALTQCKENLP SLCSXQGLRAEEN 60
 QY 61 ITESCQXRLPPAAIXISQQLIPTASASRXRXKNQAKKXEP SN 103
 DB 61 ITESCQXRLPPAAIXISQQLIPTASASRXRXKNQAKKXEP SN 103
 RESULT 6
 ID ADO71758 standard; protein; 103 AA.
 XX ADO71758;
 AC ADO71758;
 XX 09-SEP-2004 (first entry)
 DT
 XX Human selenocysteine-containing protein SEQ ID NO:2.
 DE
 XX

KW human; selenocysteine; neurotransmission; vasotropic; muscular;
 KW neuroprotective; nootropic; gastrointestinal; ophthalmological;
 KW synapse formation; erectile dysfunction; myasthenia gravis;
 KW slow channel syndrome; congenital myasthenia; Lambert Eaton syndrome;
 KW Alzheimer's disease; dementia; spino-cerebellar degeneration;
 KW autonomic imbalance; cerebral-blood-flow insufficiency;
 KW gastrointestinal disease; glaucoma.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 22
 FT /note= "selenocysteine"
 FT Modified-site 40
 FT /note= "selenocysteine"
 FT Modified-site 52
 FT /note= "selenocysteine"
 FT Modified-site 67
 FT /note= "selenocysteine"
 FT Modified-site 74
 FT /note= "selenocysteine"
 FT Modified-site 89
 FT /note= "selenocysteine"
 FT Modified-site 91
 FT /note= "selenocysteine"
 FT Modified-site 98
 FT /note= "selenocysteine"
 FT Modified-site 100
 FT /note= "selenocysteine"
 FT
 XX WO2004050114-A1.
 FN
 XX 17-JUN-2004.
 PD
 XX 28-NOV-2003; 2003WO-JP015227.
 DP
 XX 29-NOV-2002; 2002JP-00348714.
 PR
 XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
 PA
 XX Kawamura R, Naruse T, Hiraehima M, Kaminaka K, Matsuda J;
 PI Maeda H, Noda M, Wada K;
 FI WPI; 2004-461008/43.
 XX
 DR Novel agent comprising selenocysteine-containing protein capable of
 XX enhancing synapse formation, useful for improving neurotransmission
 PT failure such as myasthenia gravis or Alzheimer's disease.
 PT
 XX Disclosure; SEQ ID NO 2; 31pp; Japanese.
 PS
 XX The invention relates to a novel agent for improving neurotransmission
 CC failure, comprising selenocysteine-containing protein (seleno protein P).
 CC An agent of the invention has vasotropic, muscular, neuroprotective,
 CC nootropic, gastrointestinal, and ophthalmological activity, and acts as
 CC an enhancer of synapse formation. The agent is useful for treating
 CC neurotransmission failure such as erectile dysfunction, Lambert Eaton
 CC syndrome, slow channel syndrome, congenital myasthenia, Lambert Eaton
 CC syndrome, Alzheimer's disease, dementia, spino-cerebellar degeneration,
 CC autonomic imbalance, cerebral-blood-flow insufficiency, gastrointestinal
 CC disease or glaucoma. The present sequence represents a selenocysteine-
 CC containing protein of the invention.
 XX
 SQ Sequence 103 AA;
 Query Match 96.4%; Score 488; DB 8; Length 103;
 Best Local Similarity 100.0%; Pred. No. 6.7e-50;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPDSELA PRSXCHCHRLIFKETSALTQCKENLP SLCSXQGLRAEEN 60
 DB 1 KRCINQLLCKLPDSELA PRSXCHCHRLIFKETSALTQCKENLP SLCSXQGLRAEEN 60

QY 61 ITSCQXRLPPAAQISOQLIPTASASRXKXNOAKKXEXPSN 103
 DB 61 ITSCQXRLPPAAQISOQLIPTASASRXKXNOAKKXEXPSN 103

RESULT 7

ADP90528
 ID ADP90528 standard; protein; 103 AA.

AC ADP90528;

DT 23-SEP-2004 (first entry)

DE C-terminal human seleno protein P SeqID 2.

KW human; seleno protein P; inflammatory disease; interleukin-6; IL-6;
 KW systemic inflammatory response syndrome; thermal burn;
 KW acute pancreatitis; peritonitis; inflammatory bowel disease;
 KW organ fibrosis; malignant tumour; infectious disease; sepsis;
 KW disseminated intravascular coagulation syndrome; cell death inhibitor;
 KW antiinflammatory; vulnery; cytostatic; antimicrobial; antibacterial;
 KW immunosuppressive; anticoagulant.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 1..103
 FT /label= Xaa
 FT /note= "Xaa= selenocysteine"

PN JP2004182683-A.

XX 02-JUL-2004.

XX 05-DEC-2002; 2002JJP-00354122.

XX 05-DEC-2002; 2002JJP-00354122.

XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX WPI; 2004-473047/45.

XX Novel inflammatory disease-improving agent having seleno cysteine-
 FT containing peptide, seleno cysteine-containing protein and/or its
 FT peptide, useful for treating systemic inflammatory response syndrome.

PS Disclosure; SEQ ID NO 2; 16pp; Japanese.

XX This invention relates to a novel seleno cysteine containing peptide that
 CC can be used to treat an inflammatory disease associated with interleukin-6
 CC (IL-6) production. Specifically, it refers to a peptide that can inhibit
 CC IL-6 production that is associated with systemic inflammatory response
 CC syndrome. The present invention describes the development of
 CC pharmaceutical compositions derived from this seleno cysteine containing
 CC protein or peptide that can therefore be used for treating inflammatory
 CC diseases of external injury, thermal burns, surgical operation, and for
 CC treating acute pancreatitis, peritonitis, inflammatory bowel disease,
 CC organ fibrosis, malignant tumour, infectious disease, sepsis, systemic
 CC inflammatory response syndrome or disseminated intravascular coagulation
 CC syndrome. Accordingly, they are inhibitors of cell death and exhibit
 CC antiinflammatory, vulnery, cytostatic, antimicrobial, antibacterial,
 CC immunosuppressive and anticoagulant activities. This polypeptide sequence
 CC is the C-terminal human seleno protein P of the invention.

XX Sequence 103 AA;

Query Match 96.4%; Score 488; DB 8; Length 103;
 Best Local Similarity 100.0%; Pred. No. 6.7e-50;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINQLCKLPTDSELAPRXCCCHRLIFKTSALTCKENLPSLCSXQGLRAEN 60
 DB 1 KRCINQLCKLPTDSELAPRXCCCHRLIFKTSALTCKENLPSLCSXQGLRAEN 60

QY 61 ITSCQXRLPPAAQISOQLIPTASASRXKXNOAKKXEXPSN 103
 DB 61 ITSCQXRLPPAAQISOQLIPTASASRXKXNOAKKXEXPSN 103

RESULT 8

ADO71757

ID ADO71757 standard; protein; 362 AA.

XX ADO71757;

DT 09-SEP-2004 (first entry)

DE Human selenocysteine-containing protein SEQ ID NO:1.

KW human; selenocysteine; neurotransmission; vasotropic; muscular;
 KW neuroprotective; nootropic; gastrointestinal; ophthalmological;
 KW synapse formation; erectile dysfunction; myasthenia gravis;
 KW slow channel syndrome; congenital myasthenia; Lambert Eaton syndrome;
 KW Alzheimer's disease; dementia; spino-cerebellar degeneration;
 KW autonomic imbalance; cerebral-blood-flow insufficiency;
 KW gastrointestinal disease; glaucoma.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Modified-site 40
 FT /note= "selenocysteine"
 FT Modified-site 281
 FT /note= "selenocysteine"
 FT Modified-site 299
 FT /note= "selenocysteine"
 FT Modified-site 311
 FT /note= "selenocysteine"
 FT Modified-site 326
 FT /note= "selenocysteine"
 FT Modified-site 333
 FT /note= "selenocysteine"
 FT Modified-site 348
 FT /note= "selenocysteine"
 FT Modified-site 350
 FT /note= "selenocysteine"
 FT Modified-site 357
 FT /note= "selenocysteine"
 FT Modified-site 359
 FT /note= "selenocysteine"

PN WO2004050114-A1.

XX 17-JUN-2004.

XX 28-NOV-2003; 2003WO-JP015227.

XX 29-NOV-2002; 2002JJP-00348714.

XX (KAGA) CHEMA-SERO-THERAPEUTIC RES INST.

XX Kawamura R, Naruse T, Hirashima M, Kaminaka K, Matsuda J;
 XX Maeda H, Noda M, Wada K;

XX WPI; 2004-461008/43.

XX Novel agent comprising selenocysteine-containing protein capable of
 PT enhancing synapse formation, useful for improving neurotransmission
 PT failure such as myasthenia gravis or Alzheimer's disease.

XX Disclosure; SEQ ID NO 1; 31pp; Japanese.

XX The invention relates to a novel agent for improving neurotransmission
 CC failure, comprising selenocysteine-containing protein (seleno protein P).
 CC An agent of the invention has vasotropic, muscular, neuroprotective,
 CC nootropic, gastrointestinal, and ophthalmological activity, and acts as

CC an enhancer of synapse formation. The agent is useful for treating
 CC neurotransmission failure such as erectile dysfunction, myasthenia
 CC gravis, slow channel syndrome, congenital myasthenia, Lambert Eaton
 CC syndrome, Alzheimer's disease, dementia, spino-cerebellar degeneration,
 CC autonomic imbalance, cerebral-blood-flow insufficiency, gastrointestinal
 CC disease or glaucoma. The present sequence represents a selenocysteine-
 CC containing protein of the invention.

XX Sequence 362 AA;

Query Match 96.4%; Score 488; DB 8; Length 362;
 Best Local Similarity 100.0%; Pred. No. 2.8e-49;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLLCKLPTDSELA PRSXCHCHRLIFEKTSALTTCCKENLPSLCSXQGLRAEEN 60
 |||||
 Db 260 KRCINQLLCKLPTDSELA PRSXCHCHRLIFEKTSALTTCCKENLPSLCSXQGLRAEEN 319
 |||||
 Qy 61 ITESCQXRLPPAAQXISQQLIPTASASXRXKNQAKKXEPSPN 103
 |||||
 Db 320 ITESCQXRLPPAAQXISQQLIPTASASXRXKNQAKKXEPSPN 362
 |||||

RESULT 9

ID ADP90527 standard; protein; 362 AA.

AC ADP90527;

DT 23-SEP-2004 (first entry)

DE Human seleno protein P SeqID 1.

KW human; seleno protein P; inflammatory disease; interleukin-6; IL-6;
 KW systemic inflammatory response syndrome; thermal burn;
 KW acute pancreatitis; peritonitis; inflammatory bowel disease;
 KW organ fibrosis; malignant tumour; infectious disease; sepsis;
 KW disseminated intravascular coagulation syndrome; cell death inhibitor;
 KW antiinflammatory; vulnary; cytostatic; antimicrobial; antibacterial;
 KW immunosuppressive; anticoagulant.

OS Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 1: 362
 FT /label= Xaa
 FT /note= "Xaa= selenocysteine"

PN JP2004182683-A.

PD 02-JUL-2004.

XX '05-DEC-2002; 2002JP-00354122.

XX '05-DEC-2002; 2002JP-00354122.

PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 2004-473047/45.

PT Novel inflammatory disease-improving agent having seleno cysteine-
 PT containing peptide, seleno cysteine-containing protein and/or its
 PT peptide, useful for treating systemic inflammatory response syndrome.

PS Disclosure; SEQ ID NO 1; 16pp; Japanese.

CC This invention relates to a novel seleno cysteine containing peptide that
 CC can be used to treat an inflammatory disease associated with interleukin-6
 CC (IL-6) production. Specifically, it refers to a peptide that can inhibit
 CC IL-6 production that is associated with systemic inflammatory response
 CC syndrome. The present invention describes the development of
 CC pharmaceutical compositions derived from this seleno cysteine containing
 CC protein or peptide that can therefore be used for treating inflammatory

CC diseases of external injury, thermal burns, surgical operation, and for
 CC treating acute pancreatitis, peritonitis, inflammatory bowel disease,
 CC organ fibrosis, malignant tumour, infectious disease, sepsis, systemic
 CC inflammatory response syndrome or disseminated intravascular coagulation
 CC syndrome. Accordingly, they are inhibitors of cell death and exhibit
 CC antiinflammatory, vulnary, cytostatic, antimicrobial, antibacterial,
 CC immunosuppressive and anticoagulant activities. This polypeptide sequence
 CC is the human seleno protein P of the invention.

XX Sequence 362 AA;

Query Match 96.4%; Score 488; DB 8; Length 362;
 Best Local Similarity 100.0%; Pred. No. 2.8e-49;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLLCKLPTDSELA PRSXCHCHRLIFEKTSALTTCCKENLPSLCSXQGLRAEEN 60
 |||||
 Db 260 KRCINQLLCKLPTDSELA PRSXCHCHRLIFEKTSALTTCCKENLPSLCSXQGLRAEEN 319
 |||||
 Qy 61 ITESCQXRLPPAAQXISQQLIPTASASXRXKNQAKKXEPSPN 103
 |||||
 Db 320 ITESCQXRLPPAAQXISQQLIPTASASXRXKNQAKKXEPSPN 362
 |||||

RESULT 10

ID AAU84306 standard; protein; 381 AA.

XX AAU84306;

DT 08-MAY-2002 (first entry)

DE Human endometrial cancer related protein, SEPPI.

KW Human; endometrial cancer; differential expression; DNA microarray;
 KW protein microarray.

OS Homo sapiens.

PN WO200209573-A2.

XX 07-FEB-2002.

XX 31-JUL-2001; 2001WO-US024104.

XX 31-JUL-2000; 2000US-0221735P.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.

PI Mutter GL;

DR WPI; 2002-179967/23.

DR N-PSDB; ABK35526.

PT Diagnosing endometrial cancer comprises determining expression of nucleic
 PT acid molecules or expression products that are differentially expressed
 PT in normal and malignant endometrium.

XX Claim 33; Page 223-224; 233pp; English.

CC The invention relates to diagnosing endometrial cancer in a subject
 CC suspected of having endometrial cancer comprising determining the
 CC expression of a set of nucleic acid molecules or expression products in
 CC an endometrial sample suspected of being cancerous, where the set of
 CC nucleic acid molecules comprises at least 2 nucleic acid molecules
 CC selected from 50 fully defined sequences as given in the specification.
 CC The nucleic acids are used as an array of at least 2 of the 50 nucleic
 CC acids bound to a solid substrate. Also included is a solid-phase protein
 CC microarray comprising at least 2 antibodies or its antigen binding
 CC fragments, that specifically bind at least 2 different polypeptides from
 CC the 50 fully defined sequences as given in the specification, fixed to a
 CC solid substrate. The methods and arrays are useful for the diagnosis of
 CC endometrial cancer, selecting and monitoring treatment regimes and

CC identification of lead compounds useful for the treatment of endometrial
 CC cancer. The present sequence is one of 50 proteins differentially
 CC expressed between cancerous and non-cancerous samples
 XX
 SQ Sequence 381 AA;

Query Match 96.4%; Score 488; DB 5; Length 381;
 Best Local Similarity 100.0%; Pred. No. 3e-49;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINQLLCKLPTDSELAAPRSXCHCHRLIPEKTSALTQCKENLPSLCSXQGLRAEN 60
 DB 279 KRCINQLLCKLPTDSELAAPRSXCHCHRLIPEKTSALTQCKENLPSLCSXQGLRAEN 338
 QY 61 ITESCQRLPPAAQXISQQLIPTASASRXKKNQAKKXEPNS 103
 DB 339 ITESCQRLPPAAQXISQQLIPTASASRXKKNQAKKXEPNS 381

RESULT 11
 ABU89753
 ID ABU89753 standard; protein; 381 AA.
 AC ABU89753;
 XX
 DT 10-JUL-2003 (first entry)
 XX
 DE Protein differentially expressed in cardiovascular disease #47.
 XX
 KW Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;
 KW myocardial infarction; cardiast; antiarteriosclerotic; antianginal;
 KW gene therapy; differential gene expression.
 XX
 OS Homo sapiens.
 XX
 FN WO2003031650-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-EP011034.
 XX
 PR 08-OCT-2001; 2001GB-00024145.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Munnes M, Gehrman M, Wick M, Schmitz G;
 XX
 DR WPI; 2003-403108/38.
 DR N-PSDB; ACA89926.
 XX
 PT Predicting, diagnosing or prognosing a cardiovascular disease, e.g.
 PT angina, ischemia, myocardial infarction or arteriosclerosis by detection
 PT of a polynucleotide in a biological sample comprises detecting a
 PT hybridization complex.

PS Claim 3; Page 391-392; 454pp; English.
 XX
 CC The invention describes a method of predicting, diagnosing or prognosing
 CC a cardiovascular disease by detection of a polynucleotide in a biological
 CC sample comprising hybridising at least one of the polynucleotide to a
 CC nucleic acid material of a biological sample, thus forming a
 CC hybridisation complex, and detecting the hybridisation complex. The
 CC polynucleotides, polypeptides, antisense molecule, antibody and reagent
 CC are useful for preparing compositions for preventing, predicting or
 CC diagnosing, or a medicament for treating a cardiovascular disease, e.g.
 CC arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.
 CC This sequence represents a protein identified in the invention a being
 CC differentially expressed in individuals with cardiovascular disease
 XX
 SQ Sequence 381 AA;

Query Match 96.4%; Score 488; DB 6; Length 381;
 Best Local Similarity 100.0%; Pred. No. 3e-49;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPTDSELAAPRSXCHCHRLIPEKTSALTQCKENLPSLCSXQGLRAEN 60
 DB 279 KRCINQLLCKLPTDSELAAPRSXCHCHRLIPEKTSALTQCKENLPSLCSXQGLRAEN 338
 QY 61 ITESCQRLPPAAQXISQQLIPTASASRXKKNQAKKXEPNS 103
 DB 339 ITESCQRLPPAAQXISQQLIPTASASRXKKNQAKKXEPNS 381

RESULT 12
 ADP65180
 ID ADP65180 standard; protein; 381 AA.
 AC ADP65180;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human selenoprotein P precursor.
 XX
 KW autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.
 XX
 OS Homo sapiens.
 XX
 FN WO2003072827-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 31-OCT-2002; 2002WO-US035433.
 XX
 PR 31-OCT-2001; 2001US-0336220P.
 XX
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 PI Hirech R, Thorton SL;
 XX
 DR WPI; 2003-712740/67.
 DR GENBANK; NP_005401.
 XX
 PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.

PS Disclosure; Page; 56pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; or
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, and
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an

CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIFO.

XX SQ Sequence 381 AA;

Query Match 96.4%; Score 488; DB 7; Length 381;
 Best Local Similarity 91.3%; Pred. No. 3e-49;
 Matches 94; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPTDSELAAPRSXCHCHRLIFEKTSALTVOCKENLPSLCSVQGLRAEN 60
 DB 279 KRCINQLLCKLPTDSELAAPRSXCHCHRLIFEKTSALTVOCKENLPSLCSVQGLRAEN 338

QY 61 ITESCQVRLPPAAVQISQQLIPTASASXRXKNOAKKXEPSN 103
 DB 339 ITESCQVRLPPAAVQISQQLIPTASASXRXKNOAKKXEPSN 381

RESULT 13

ADN95151 ID ADN95151 standard; protein; 380 AA.

XX AC ADN95151;

XX DT 01-JUL-2004 (first entry)

XX DE Human BEC/LEC-related protein sequence SeqID73.

XX KW growth; differentiation; blood endothelial cell; BEC;
 KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
 KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
 KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
 KW inflammatory disease; cancer metastasis; lymphatic system; human.

XX OS Homo sapiens.

XX PN WO2003080640-A1.

XX PD 02-OCT-2003.

XX PF 07-MAR-2003; '2003WO-US006900.

XX PR 07-MAR-2002; 2002US-0363019P.

XX FA (LUDW-) LUDWIG INST CANCER RES.

XX PA (LICN) LICENTIA LTD.

XX PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;

XX DR WPI, 2003-876899/81.

XX DR N-PSDB; ADN95152.

XX PS Example 1; SEQ ID NO 73; 176pp; English.

CC This invention relates to a method of differentially modulating the
 CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
 CC endothelial cells (LEC) comprises contacting endothelial cells with a
 CC composition comprising an agent that differentially modulates blood or
 CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
 CC identifying a human subject with lymphoedema and with a mutation in at
 CC least one allele of a gene encoding a LEC protein, where the mutation
 CC correlates with lymphoedema in human subjects, and with the proviso that
 CC the LEC protein is not VEGFR-3; and administering to the subject a
 CC composition comprising a lymphatic growth agent selected from VEGF-C or
 CC VEGF-D polypeptides and polynucleotides. The invention may be useful for
 CC the development of compounds with an antiangiogenic, cytostatic,
 CC vasotropic or antiinflammatory activity or for gene therapy. The method
 CC is useful in modulating the growth or differentiation of blood
 CC endothelial cells or lymphatic endothelial cells, in treating hereditary
 CC lymphoedema, in screening for an endothelial cell disorder or

CC predisposition to the disorder or in monitoring the efficacy or toxicity
 CC of a drug on endothelial cells. The agent is useful in manufacturing a
 CC medicament for the differential modulation of blood vessel endothelial
 CC cell or lymphatic vessel endothelial cell growth or differentiation. The
 CC lymphatic growth agent may also be used in manufacturing a medicament for
 CC the treatment of hereditary lymphoedema resulting from a mutation in a
 CC LEC gene or of other diseases involving the lymphatic vessels, such as
 CC various inflammatory diseases and cancer metastasis via the lymphatic
 CC system. The present sequence is that of a human LEC/BEC differentially
 CC expressed protein which is related to the method of the invention. Note:
 CC This sequence does not appear in the specification but was obtained by
 CC the indexer using the source data given in table 14 of the specification.

XX SQ Sequence 380 AA;

Query Match 95.3%; Score 482; DB 7; Length 380;
 Best Local Similarity 91.2%; Pred. No. 1.5e-48;
 Matches 93; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPTDSELAAPRSXCHCHRLIFEKTSALTVOCKENLPSLCSVQGLRAEN 60
 DB 279 KRCINQLLCKLPTDSELAAPRSXCHCHRLIFEKTSALTVOCKENLPSLCSVQGLRAEN 338

QY 61 ITESCQVRLPPAAVQISQQLIPTASASXRXKNOAKKXEPS 102

DB 339 ITESCQVRLPPAAVQISQQLIPTASASXRXKNOAKKXEPS 380

RESULT 14

AAB03185

ID AAB03185 standard; peptide; 103 AA.

XX AC AAB03185;

XX DT 23-OCT-2000 (first entry)

XX DE Human selenoprotein P C-terminal 103 residues.

XX KW Selenoprotein P fragment; human; programmed cell death inhibitor;
 KW apoptosis inhibitor; antiapoptotic; acquired immunodeficiency syndrome;
 KW AIDS; Parkinson's disease; Alzheimer's disease; myocardial infarct;
 KW cerebral infarct; stroke; reperfusion injury; organ transplant rejection;
 KW arteriosclerosis; redox disorder; immune disorder; cardiovascular;
 KW cerebroprotective; culture medium additive.

XX OS Homo sapiens.

Key	Location/Qualifiers
Modified-site 22	/note= "Selenocysteine"
Modified-site 40	/note= "Selenocysteine"
Modified-site 52	/note= "Selenocysteine"
Modified-site 67	/note= "Selenocysteine"
Modified-site 74	/note= "Selenocysteine"
Modified-site 89	/note= "Selenocysteine"
Modified-site 91	/note= "Selenocysteine"
Modified-site 98	/note= "Selenocysteine"
Modified-site 100	/note= "Selenocysteine"

WO2000031131-A1.

02-JUN-2000.

12-NOV-1999; 99WO-JP006322.

XX

```

PR 19-NOV-1998; 98JP-00347863.
XX (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
XX Hirashima M, Maeda H, Nozaki C;
XX
XX WPI; 2000-451677/39.
XX
XX Peptide fragments with cell death inhibitory activity, useful in
XX preventing and treating apoptosis-associated diseases particularly caused
XX by stress e.g. Parkinson's disease, Alzheimer's and arteriosclerosis.
XX
XX Disclosure; Page 11; 56pp; Japanese.
XX
XX The invention relates to fragments (AAB03183, AAB03184) derived from the
XX C-terminal 103 amino acids of human selenoprotein P (AAB03188) which act
XX as inhibitors of apoptosis (programmed cell death), their use in
XX therapeutic compositions and cell culture media, and antibodies against
XX them. The invention also relates to a method for studying the phenomenon
XX of sudden cell death in a human megakaryotic series gemmule cell culture
XX system involving use of the anti-apoptotic peptides of the invention.
XX Selenoprotein P is a plasma protein which confers protection against
XX peroxynitrite-mediated oxidation and nitration. The peptide fragments can
XX be used as prophylactic and therapeutic agents for apoptosis-associated
XX diseases, including AIDS (acquired immunodeficiency syndrome),
XX Parkinson's disease, Alzheimer's disease, arteriosclerosis, myocardial
XX infarct, cerebral infarct, organ transplant rejection, and reperfusion
XX injury. They may also be used in the prevention or treatment of disorders
XX relating to redox reactions, or of disorders of the immune system. They
XX may additionally be used as an additive for cell culture and for
XX screening cell death activity in vitro. The present sequence represents
XX the C-terminal 103 amino acids of human selenoprotein P
XX
XX Sequence 103 AA;
XX
XX Query Match 94.7%; Score 479; DB 3; Length 103;
XX Best Local Similarity 91.3%; Pred. No. 7.8e-49;
XX Matches 94; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX 1 KRCINQLLCKLPTDSELAPRSXKCHRHILFEKTSAITXQCKENLPSLCXQGLRAEN 60
XX 1 KRCINQLLCKLPTDSELAPRSXKCHRHILFEKTSAITXQCKENLPSLCXQGLRAEN 60
XX
XX 61 ITESCQXRLPPAAXQISQOLIPTASASXRXKNQAKKXEPSN 103
XX 61 ITESCQXRLPPAAXQISQOLIPTASASXRXKNQAKKXEPSN 103
XX
XX RESULT 15
XX AAB03188
XX ID AAB03188 standard; peptide; 381 AA.
XX
XX AC AAB03188;
XX
XX 23-OCT-2000 (first entry)
XX
XX Human selenoprotein P.
XX
XX Selenoprotein P; human; programmed cell death inhibitor;
XX apoptosis inhibitor; antiapoptotic; acquired immunodeficiency syndrome;
XX AIDS; Parkinson's disease; Alzheimer's disease; myocardial infarct;
XX cerebral infarct; stroke; reperfusion injury; organ transplant rejection;
XX arteriosclerosis; redox disorder; immune disorder; cardiovascular;
XX cerebroprotective; culture medium additive.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Peptide 1..19
XX FT Protein /note= "Signal peptide"
XX FT Protein 19..381
XX FT Modified-site /note= "Mature human selenoprotein P"
XX 281

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FT Modified-site /note= "Selenocysteine"
FT 299
FT Modified-site /note= "Selenocysteine"
FT 311
FT Modified-site /note= "Selenocysteine"
FT 326
FT Modified-site /note= "Selenocysteine"
FT 333
FT Modified-site /note= "Selenocysteine"
FT 348
FT Modified-site /note= "Selenocysteine"
FT 350
FT Modified-site /note= "Selenocysteine"
FT 357
FT Modified-site /note= "Selenocysteine"
FT 359
FT Modified-site /note= "Selenocysteine"
XX WO200031131-A1.
XX
XX 02-JUN-2000.
XX
XX 12-NOV-1999; 99WO-JP006322.
XX
XX 19-NOV-1998; 98JP-00347863.
XX (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
XX Hirashima M, Maeda H, Nozaki C;
XX
XX WPI; 2000-451677/39.
XX
XX Peptide fragments with cell death inhibitory activity, useful in
XX preventing and treating apoptosis-associated diseases particularly caused
XX by stress e.g. Parkinson's disease, Alzheimer's and arteriosclerosis.
XX
XX Example 3; Page 20; 56pp; Japanese.
XX
XX The invention relates to fragments (AAB03183, AAB03184) derived from the
XX C-terminal 103 amino acids of human selenoprotein P (AAB03188) which act
XX as inhibitors of apoptosis (programmed cell death), their use in
XX therapeutic compositions and cell culture media, and antibodies against
XX them. The invention also relates to a method for studying the phenomenon
XX of sudden cell death in a human megakaryotic series gemmule cell culture
XX system involving use of the anti-apoptotic peptides of the invention.
XX Selenoprotein P is a plasma protein which confers protection against
XX peroxynitrite-mediated oxidation and nitration. The peptide fragments can
XX be used as prophylactic and therapeutic agents for apoptosis-associated
XX diseases, including AIDS (acquired immunodeficiency syndrome),
XX Parkinson's disease, Alzheimer's disease, arteriosclerosis, myocardial
XX infarct, cerebral infarct, organ transplant rejection, and reperfusion
XX injury. They may also be used in the prevention or treatment of disorders
XX relating to redox reactions, or of disorders of the immune system. They
XX may additionally be used as an additive for cell culture and for
XX screening cell death activity in vitro. The present sequence represents
XX human selenoprotein P
XX
XX Sequence 381 AA;
XX
XX Query Match 94.7%; Score 479; DB 3; Length 381;
XX Best Local Similarity 91.3%; Pred. No. 3.5e-48;
XX Matches 94; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX 1 KRCINQLLCKLPTDSELAPRSXKCHRHILFEKTSAITXQCKENLPSLCXQGLRAEN 60
XX 1 KRCINQLLCKLPTDSELAPRSXKCHRHILFEKTSAITXQCKENLPSLCXQGLRAEN 388
XX
XX 61 ITESCQXRLPPAAXQISQOLIPTASASXRXKNQAKKXEPSN 103
XX 61 ITESCQXRLPPAAXQISQOLIPTASASXRXKNQAKKXEPSN 381
XX
XX 339 ITESCQXRLPPAAXQISQOLIPTASASXRXKNQAKKXEPSN 381
XX
XX Search completed: April 15, 2005, 10:10:30

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Job time : 174 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 09:50:19 ; Search time 42 Seconds
(without alignments)
183.068 Million cell updates/sec

Title: US-09-856-199-3

Perfect score: 506

Sequence: 1 KRCINQLLCKLPTDSELA.....EASASXXKXKQAKXEPSPN 103

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	96.4	381	4	US-09-919-497-96
2	111	21.9	110	4	US-09-513-999C-7836
3	68.5	13.5	358	3	US-08-915-795-8
4	68.5	13.5	358	4	US-09-847-524-2
5	68.5	13.5	358	4	US-09-296-275-8
6	68.5	13.5	358	4	US-09-438-046-15
7	67.5	13.3	104	4	US-09-214-982-28
8	67.5	13.3	325	3	US-08-915-795-3
9	67.5	13.3	325	4	US-09-296-275-3
10	67.5	13.3	354	3	US-08-915-795-5
11	67.5	13.3	354	4	US-09-296-275-5
12	67.5	13.3	354	4	US-09-375-248-6
13	67.5	13.3	354	4	US-09-468-647A-109
14	67.5	13.3	354	4	US-09-169-079-22
15	67.5	13.3	354	4	US-09-214-982-1
16	67.5	13.3	362	4	US-09-949-016-11286
17	67.5	13.3	422	4	US-09-949-016-11379
18	67.5	13.3	1385	4	US-09-827-998-16
19	67.5	13.3	1770	4	US-09-827-998-10
20	67.5	13.3	1791	4	US-09-827-998-3
21	66	13.0	289	4	US-09-252-991A-32560
22	65.5	12.9	442	4	US-09-579-692B-58
23	65.5	12.9	604	2	US-08-511-485-6
24	65.5	12.9	604	3	US-09-212-971-6
25	65.5	12.9	604	3	US-08-800-929A-6
26	65.5	12.9	604	3	US-08-569-749-4
27	65.5	12.9	604	3	US-09-617-053A-6

28	65.5	12.9	604	4	US-09-201-936-6	Sequence 6, Appli
29	65.5	12.9	604	4	US-09-011-356-6	Sequence 6, Appli
30	65.5	12.9	604	4	US-09-672-717-221	Sequence 221, Appl
31	65.5	12.9	604	4	US-09-201-932-6	Sequence 6, Appli
32	65.5	12.9	604	4	US-09-949-016-6031	Sequence 6031, Ap
33	65.5	12.9	604	4	US-09-689-366-4	Sequence 4, Appli
34	65.5	12.9	604	5	PCT-US96-12860-4	Sequence 4, Appli
35	65.5	12.9	613	4	US-09-949-016-10878	Sequence 10878, A
36	65.5	12.9	1140	4	US-09-579-692B-8	Sequence 8, Appli
37	65	12.8	1009	4	US-09-762-724-10	Sequence 10, Appl
38	64	12.6	191	4	US-09-489-039A-11356	Sequence 11356, A
39	63.5	12.5	165	4	US-09-270-767-46489	Sequence 46489, A
40	63.5	12.5	257	4	US-09-252-991A-31359	Sequence 31359, A
41	63.5	12.5	716	2	US-08-766-982-1	Sequence 1, Appli
42	63.5	12.5	716	3	US-09-296-219-1	Sequence 1, Appli
43	63	12.5	1022	4	US-09-949-016-10242	Sequence 10242, A
44	63	12.5	4302	3	US-08-658-136-5	Sequence 5, Appli
45	62.5	12.4	1220	1	US-08-158-232-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-919-497-96
; Sequence 96, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (59)..(59)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (300)..(300)
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; LOCATION: (330)..(330)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (345)..(345)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (352)..(352)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (367)..(367)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (369)..(369)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (376)..(376)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (378)..(378)
; OTHER INFORMATION: Xaa = any amino acid
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Query Match 96.4%; Score 488; DB 4; Length 381;
Best Local Similarity 100.0%; Pred. No. 8.8e-54;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLCKLPTDSELAPRSCXCHCHRLIFKTSALTCKENLPSLCSXQGLRAEN 60
Db KRCINQLCKLPTDSELAPRSCXCHCHRLIFKTSALTCKENLPSLCSXQGLRAEN 338

Qy 61 ITESQXRLPAAQISOILPTASASRXKNOAKKXEPN 103
Db ITESQXRLPAAQISOILPTASASRXKNOAKKXEPN 381

RESULT 2
US-09-513-999C-7836
; Sequence 7836, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7836
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -24...-1
; OTHER INFORMATION: score 4.7
; OTHER INFORMATION: seq LLMIKSTAAATRS/SR
US-09-513-999C-7836

Query Match 21.9%; Score 111; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLCKLPTDSELAPRS 21
Db 90 KRCINQLCKLPTDSELAPRS 110

RESULT 3
US-08-915-795-8
; Sequence 8, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
TISSUE TYPE: Mouse Lung
US-08-915-795-8

Query Match 13.5%; Score 68.5; DB 3; Length 358;
Best Local Similarity 27.5%; Pred. No. 1.7;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;

Qy 2 RCINQLCKLPTDSELAPRSXCHCHRLIFKTSALTCKENLPSLCSXQGLRAENI 61
Db 273 RC--ECVCKAPCPGDLIQHPNCSC-----FECKESLSCCCKHKIFHPD-- 315

Qy 62 TESQXRLP 70
Db 316 TCSCEDRCP 324

RESULT 4
US-09-847-524-2
; Sequence 2, Application US/09847524
; Patent No. 6689352
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G
; APPLICANT: STACKER, Steven A
; TITLE OF INVENTION: A METHOD FOR ACTIVATING ONLY THE VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR RECEPTOR-3 AND USES THEREOF
; FILE REFERENCE: Achen&Stacker-mouse VEGF-D
; CURRENT APPLICATION NUMBER: US/09/847,524
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-847-524-2

Query Match 13.5%; Score 68.5; DB 4; Length 358;
Best Local Similarity 27.5%; Pred. No. 1.7;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;

Qy 2 RCINQLCKLPTDSELAPRSXCHCHRLIFKTSALTCKENLPSLCSXQGLRAENI 61
Db 273 RC--ECVCKAPCPGDLIQHPNCSC-----FECKESLSCCCKHKIFHPD-- 315

Qy 62 TESQXRLP 70
Db 316 TCSCEDRCP 324

RESULT 5
US-09-296-275-8
; Sequence 8, Application US/09296275

Patent No. 6689580
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/296,275
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/915,795
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
TISSUE TYPE: Mouse Lung
US-09-296-275-8
Query Match 13.5%; Score 68.5; DB 4; Length 358;
Best Local Similarity 27.5%; Pred. No. 1.7;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;
QY 2 RCINQLLCKLPDSELPASXCCHRHILFEKTSAITXQCKENLPISCSXQGLRAENI 61
DB 273 RC--ECVCKAPCGDLIQHPENCSC-----FECKESLESCCKHKIFHPD-- 315
QY 62 TESCOXRLP 70
DB 316 TCSCEDRCP 324
RESULT 6
US-09-438-046-15
Sequence 15, Application US/09438046
Patent No. 6706687
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING

TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: Ulf Eriksson et al 1064-44833
CURRENT APPLICATION NUMBER: US/09/438,046
CURRENT FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/150,604
EARLIER FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 15
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-09-438-046-15

Query Match 13.5%; Score 68.5; DB 4; Length 358;
Best Local Similarity 27.5%; Pred. No. 1.7;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;
QY 2 RCINQLLCKLPDSELPASXCCHRHILFEKTSAITXQCKENLPISCSXQGLRAENI 61
DB 273 RC--ECVCKAPCGDLIQHPENCSC-----FECKESLESCCKHKIFHPD-- 315
QY 62 TESCOXRLP 70
DB 316 TCSCEDRCP 324

RESULT 7
US-09-214-982-28
Sequence 28, Application US/09214982
Patent No. 6828426
GENERAL INFORMATION:
APPLICANT: Hirata, Yuichi
APPLICANT: Nezu, Junichi
TITLE OF INVENTION: No. 6828426el VEGF-like Factor
FILE REFERENCE: 50026/014001
CURRENT APPLICATION NUMBER: US/09/214,982
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 8-185216 Japan
EARLIER FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 104
TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-982-28

Query Match 13.3%; Score 67.5; DB 4; Length 104;
Best Local Similarity 27.5%; Pred. No. 0.5;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;
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DB 18 RC--ECVCKTFCPKDLIQHPKNCSC-----FECKESLESCCKHKIFHPD-- 60
QY 62 TESCOXRLP 70
DB 61 TCSCEDRCP 69

RESULT 8
US-08-915-795-3
Sequence 3, Application US/08915795
Patent No. 6235713

GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
US-08-915-795-3
Query Match 13.3%; Score 67.5; DB 3; Length 325;
Best Local Similarity 27.5%; Pred. No. 2;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;
Qy 2 RCINQLCKLPDSELPKRSXCCHRLIFEKTSAITXCKENLPSLCSXQGLRAENI 61
Db 239 RC--ECVCKTPCKDLIHPKNCSC-----FECKESLETCCQKHKLPHDP-- 281
Qy 62 TESCQXRLP 70
Db 282 TCSCEDRCP 290
RESULT 9
US-09-296-275-3
Sequence 3, Application US/09296275
Patent No. 6689580
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/296,275
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/915,795
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
US-09-296-275-3
Query Match 13.3%; Score 67.5; DB 4; Length 325;
Best Local Similarity 27.5%; Pred. No. 2;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;
Qy 2 RCINQLCKLPDSELPKRSXCCHRLIFEKTSAITXCKENLPSLCSXQGLRAENI 61
Db 239 RC--ECVCKTPCKDLIHPKNCSC-----FECKESLETCCQKHKLPHDP-- 281
Qy 62 TESCQXRLP 70
Db 282 TCSCEDRCP 290
RESULT 10
US-08-915-795-5
Sequence 5, Application US/08915795
Patent No. 6235713
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536


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; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
; US-08-915-795-5

Query Match 13.3%; Score 67.5; DB 3; Length 354;
Best Local Similarity 27.5%; Pred. No. 2.2;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;

QY 2 RCINQLLCKLPDSELA PRSXCHRH LIFKTSAITXQCKENLP SLCSXQGLRAENI 61
Db 268 RC--ECVCKTPCKDLIQHPKNCSC-----FECKESLETCCQKHLPHPD-- 310

QY 62 TESCOXRLP 70
Db 311 TCSCEDRCP 319

RESULT 11
US-09-296-275-5
; Sequence 5, Application US/09296275
; Patent No. 6689580
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/296,275
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/915,795
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
; US-09-296-275-5

Query Match 13.3%; Score 67.5; DB 4; Length 354;
Best Local Similarity 27.5%; Pred. No. 2.2;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;

QY 2 RCINQLLCKLPDSELA PRSXCHRH LIFKTSAITXQCKENLP SLCSXQGLRAENI 61
Db 268 RC--ECVCKTPCKDLIQHPKNCSC-----FECKESLETCCQKHLPHPD-- 310

QY 62 TESCOXRLP 70
Db 311 TCSCEDRCP 319

RESULT 12
US-09-375-248-6
; Sequence 6, Application US/09375248
; Patent No. 6764820
; GENERAL INFORMATION:
; APPLICANT: Ferrell, Robert E.
; APPLICANT: Alitalo, Kari
; APPLICANT: Pinesgold, David N.
; APPLICANT: Karikainen, Marika
; TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
; FILE REFERENCE: 28967/35255A
; CURRENT APPLICATION NUMBER: US/09/375,248
; CURRENT FILING DATE: 1999-08-16
; EARLIER APPLICATION NUMBER: PCT/US99/06133
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-375-248-6

Query Match 13.3%; Score 67.5; DB 4; Length 354;
Best Local Similarity 27.5%; Pred. No. 2.2;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;

QY 2 RCINQLLCKLPDSELA PRSXCHRH LIFKTSAITXQCKENLP SLCSXQGLRAENI 61
Db 268 RC--ECVCKTPCKDLIQHPKNCSC-----FECKESLETCCQKHLPHPD-- 310

QY 62 TESCOXRLP 70
Db 311 TCSCEDRCP 319

RESULT 13
US-09-468-647A-109
; Sequence 109, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Yon, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiewska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
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FILE REFERENCE: B0192.70011US00
CURRENT APPLICATION NUMBER: US/09/468,647A
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: GB 9828377.3
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/124,967
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: US 60/164,131
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.2
SEQ ID NO 109
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens
US-09-468-647A-109

Query Match 13.3%; Score 67.5; DB 4; Length 354;
Best Local Similarity 27.5%; Pred. No. 2.2;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;
Qy 2 RCINOLLCKLPDSELAPRSXCCHRHILFEKTSAITXOCKENLPSLCSXQGLRAEENI 61
Db 268 RC--ECVCKTPCKDLIQHPKNCSC-----FECKESLETCCQKHKLPHDP-- 310
Qy 62 TESQXRLP 70
Db 311 TCSCEDRCP 319

RESULT 14
US-09-169-079-22
Sequence 22, Application US/09169079
Patent No. 6824777
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kaipainen, Arja
APPLICANT: Valtola, Reija
APPLICANT: Jussila, Lotta
TITLE OF INVENTION: Fit4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Thera
FILE REFERENCE: 28113/34891
CURRENT APPLICATION NUMBER: US/09/169,079
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: 08/901,710
EARLIER FILING DATE: 1997-07-28
EARLIER APPLICATION NUMBER: 08/340,011
EARLIER FILING DATE: 1994-11-14
EARLIER APPLICATION NUMBER: 08/257,754
EARLIER FILING DATE: 1994-07-09
EARLIER APPLICATION NUMBER: 07/959,951
EARLIER FILING DATE: 1992-10-09
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens
US-09-169-079-22

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Best Local Similarity 27.5%; Pred. No. 2.2;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;
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Db 268 RC--ECVCKTPCKDLIQHPKNCSC-----FECKESLETCCQKHKLPHDP-- 310
Qy 62 TESQXRLP 70
Db 311 TCSCEDRCP 319

RESULT 15

US-09-214-982-1
Sequence 1, Application US/09214982
Patent No. 6828426
GENERAL INFORMATION:
APPLICANT: Hirata, Yuichi
APPLICANT: Nezu, Junichi
TITLE OF INVENTION: NO. 6828426el VEGF-like Factor
FILE REFERENCE: 50026/014001
CURRENT APPLICATION NUMBER: US/09/214,982
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 8-185216 Japan
EARLIER FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-982-1

Query Match 13.3%; Score 67.5; DB 4; Length 354;
Best Local Similarity 27.5%; Pred. No. 2.2;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;
Qy 2 RCINOLLCKLPDSELAPRSXCCHRHILFEKTSAITXOCKENLPSLCSXQGLRAEENI 61
Db 268 RC--ECVCKTPCKDLIQHPKNCSC-----FECKESLETCCQKHKLPHDP-- 310
Qy 62 TESQXRLP 70
Db 311 TCSCEDRCP 319

Search completed: April 15, 2005, 10:12:09
Job time : 43 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 10:10:39 ; Search time 131 Seconds
(without alignments)
261.330 Million cell updates/sec

Title: US-09-856-199-3
Perfect score: 506
Sequence: 1 KRCINQLLCKLPTDSELAPR.....EASASRXRNQAKXKXPSN 103

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	488	96.4	103	17	US-10-472-444-3 Sequence 3, Appli
2	488	96.4	381	9	US-09-919-497-96 Sequence 96, Appl
3	182	36.0	33	17	US-10-472-444-4 Sequence 4, Appli
4	162	32.0	29	17	US-10-472-444-1 Sequence 1, Appli
5	132	25.1	28	17	US-10-472-444-2 Sequence 2, Appli
6	111	21.9	21	17	US-10-472-444-5 Sequence 5, Appli
7	111	21.9	240	9	US-09-925-300-1658 Sequence 1658, Ap
8	111	21.9	299	15	US-10-210-172-20 Sequence 20, Appl
9	81	16.0	131	16	US-10-437-963-126312 Sequence 126312,
10	72.5	14.3	792	13	US-10-087-192-1977 Sequence 1977, Ap
11	69	13.6	128	9	US-09-864-761-35896 Sequence 35896, A
12	68.5	13.5	358	10	US-09-852-203A-13 Sequence 13, Appl
13	68.5	13.5	358	10	US-09-847-524-2 Sequence 2, Appli

14	68.5	13.5	358	13	US-10-139-876-2	Sequence 2, Appli
15	68.5	13.5	358	14	US-10-131-600-13	Sequence 13, Appl
16	68.5	13.5	358	14	US-10-274-953-8	Sequence 8, Appli
17	68.5	13.5	358	14	US-10-161-694-8	Sequence 8, Appli
18	68.5	13.5	358	15	US-10-303-997B-13	Sequence 13, Appl
19	68.5	13.5	358	15	US-10-439-337A-13	Sequence 13, Appl
20	68.5	13.5	358	15	US-10-705-476-8	Sequence 8, Appli
21	67.5	13.3	128	15	US-10-424-599-263417	Sequence 263417,
22	67.5	13.3	325	14	US-10-274-953-3	Sequence 3, Appli
23	67.5	13.3	325	14	US-10-161-694-3	Sequence 3, Appli
24	67.5	13.3	325	16	US-10-705-476-3	Sequence 3, Appli
25	67.5	13.3	354	9	US-09-956-095-2	Sequence 2, Appli
26	67.5	13.3	354	9	US-09-219-345A-11	Sequence 11, Appl
27	67.5	13.3	354	9	US-09-795-006A-119	Sequence 119, App
28	67.5	13.3	354	10	US-09-375-248-6	Sequence 6, Appli
29	67.5	13.3	354	11	US-09-765-534B-22	Sequence 22, Appl
30	67.5	13.3	354	14	US-10-262-538-26	Sequence 26, Appl
31	67.5	13.3	354	14	US-10-274-953-5	Sequence 5, Appli
32	67.5	13.3	354	14	US-10-161-694-5	Sequence 5, Appli
33	67.5	13.3	354	15	US-10-661-740-6	Sequence 6, Appli
34	67.5	13.3	354	16	US-10-705-476-5	Sequence 5, Appli
35	67.5	13.3	354	17	US-10-868-577A-4	Sequence 4, Appli
36	67.5	13.3	354	17	US-10-868-549-4	Sequence 4, Appli
37	67.5	13.3	362	13	US-10-139-876-4	Sequence 4, Appli
38	67.5	13.3	526	13	US-10-087-192-2016	Sequence 2016, Ap
39	67.5	13.3	1385	9	US-09-827-998-16	Sequence 16, Appl
40	67.5	13.3	1385	15	US-10-675-685-16	Sequence 16, Appl
41	67.5	13.3	1770	9	US-09-827-998-10	Sequence 10, Appl
42	67.5	13.3	1770	15	US-10-675-685-10	Sequence 10, Appl
43	67.5	13.3	1791	9	US-09-827-998-3	Sequence 3, Appli
44	67.5	13.3	1791	10	US-09-983-025-2	Sequence 2, Appli
45	67.5	13.3	1791	15	US-10-675-685-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-472-444-3
; Sequence 3, Application US/10472444
; Publication No. US20050037954M1
; GENERAL INFORMATION:
; APPLICANT: HIRASHIMA, Masaki et al.
; TITLE OF INVENTION: NOVEL MEDICAMENT FOR AMERLIORATING DYSKINESIA
; FILE REFERENCE: 0020-5180P
; CURRENT APPLICATION NUMBER: US/10/472,444
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: JP 2001-84050
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
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; NAME/KEY: misc feature
; LOCATION: (22)..(22)
; OTHER INFORMATION: Xaa represents selenocysteine
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; LOCATION: (67)..(67)
; OTHER INFORMATION: Xaa represents selenocysteine
; FEATURE:
; NAME/KEY: misc feature

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (91)..(91)
; OTHER INFORMATION: Xaa represents selenocysteine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98)..(98)
; OTHER INFORMATION: Xaa represents selenocysteine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (100)..(100)
; OTHER INFORMATION: Xaa represents selenocysteine
US-10-472-444-3

```

```

Query Match          96.4%; Score 488; DB 17; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.3e-49;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLLCKLPTDSELAPRSXCCHCHRLIFKGTGSAITXCKENLPSLCSXQGLRAEEN 60
Db 1 KRCINQLLCKLPTDSELAPRSXCCHCHRLIFKGTGSAITXCKENLPSLCSXQGLRAEEN 60

Qy 61 ITESCQXRLPPAAQISQQLIPTASASRXKXKQAKKXEPSPN 103
Db 61 ITESCQXRLPPAAQISQQLIPTASASRXKXKQAKKXEPSPN 103

```

```

RESULT 2
US-09-919-497-96
; Sequence 96, Application US/09919497
; Patent No. US2002010662A1
; GENERAL INFORMATION:
; APPLICANT: Muttter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (59)..(59)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (300)..(300)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (318)..(318)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (330)..(330)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (345)..(345)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (352)..(352)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (367)..(367)
; OTHER INFORMATION: Xaa = any amino acid

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; NAME/KEY: UNSURE
; LOCATION: (369)..(369)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (376)..(376)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (378)..(378)
; OTHER INFORMATION: Xaa = any amino acid
US-09-919-497-96

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Query Match          96.4%; Score 488; DB 9; Length 381;
Best Local Similarity 100.0%; Pred. No. 6e-49;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLLCKLPTDSELAPRSXCCHCHRLIFKGTGSAITXCKENLPSLCSXQGLRAEEN 60
Db 279 KRCINQLLCKLPTDSELAPRSXCCHCHRLIFKGTGSAITXCKENLPSLCSXQGLRAEEN 338

Qy 61 ITESCQXRLPPAAQISQQLIPTASASRXKXKQAKKXEPSPN 103
Db 339 ITESCQXRLPPAAQISQQLIPTASASRXKXKQAKKXEPSPN 381

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RESULT 3
US-10-472-444-4
; Sequence 4, Application US/10472444
; Publication No. US20050037954A1
; GENERAL INFORMATION:
; APPLICANT: HIRASHIMA, Masaki et al.
; TITLE OF INVENTION: NOVEL MEDICAMENT FOR AMERLIORATING DYSKINESIA
; FILE REFERENCE: 0020-5180P
; CURRENT APPLICATION NUMBER: US/10/472,444
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: JP 2001-84050
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22)..(22)
; OTHER INFORMATION: Xaa represents selenocysteine
US-10-472-444-4

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```

Query Match          36.0%; Score 182; DB 17; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.8e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLLCKLPTDSELAPRSXCCHCHRLIFK 33
Db 1 KRCINQLLCKLPTDSELAPRSXCCHCHRLIFK 33

```

```

RESULT 4
US-10-472-444-1
; Sequence 1, Application US/10472444
; Publication No. US20050037954A1
; GENERAL INFORMATION:
; APPLICANT: HIRASHIMA, Masaki et al.
; TITLE OF INVENTION: NOVEL MEDICAMENT FOR AMERLIORATING DYSKINESIA
; FILE REFERENCE: 0020-5180P
; CURRENT APPLICATION NUMBER: US/10/472,444
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: JP 2001-84050
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 29

```

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22)..(22)
; OTHER INFORMATION: Xaa represents selenocysteine
US-10-472-444-1

Query Match      32.0%; Score 162; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.4e-12;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLLCKLPTDSELAPRSXCCHRH 29
Db 1 KRCINQLLCKLPTDSELAPRSXCCHRH 29

RESULT 5
US-10-472-444-2
; Sequence 2, Application US/10472444
; Publication No. US20050037954A1
; GENERAL INFORMATION:
; APPLICANT: HIRASHIMA, Masaki et al.
; TITLE OF INVENTION: NOVEL MEDICAMENT FOR AMERLIORATING DYSKINESIA
; FILE REFERENCE: 0020-5180P
; CURRENT APPLICATION NUMBER: US/10/472,444
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: JP 2001-84050
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: Xaa represents selenocysteine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: Xaa represents selenocysteine
US-10-472-444-2

Query Match      26.1%; Score 132; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 TGSALTXXCKENLPSCXQGLRAENI 61
Db 1 TGSALTXXCKENLPSCXQGLRAENI 28

RESULT 6
US-10-472-444-5
; Sequence 5, Application US/10472444
; Publication No. US20050037954A1
; GENERAL INFORMATION:
; APPLICANT: HIRASHIMA, Masaki et al.
; TITLE OF INVENTION: NOVEL MEDICAMENT FOR AMERLIORATING DYSKINESIA
; FILE REFERENCE: 0020-5180P
; CURRENT APPLICATION NUMBER: US/10/472,444
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: JP 2001-84050
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-472-444-5

Query Match      21.9%; Score 111; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLLCKLPTDSELAPRS 21
Db 1 KRCINQLLCKLPTDSELAPRS 21

RESULT 7
US-09-925-300-1658
; Sequence 1658, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Steve Ruben
; APPLICANT: Craig Rosen
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1658
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1658

Query Match      21.9%; Score 111; DB 9; Length 240;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLLCKLPTDSELAPRS 21
Db 220 KRCINQLLCKLPTDSELAPRS 240

RESULT 8
US-10-210-172-20
; Sequence 20, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vermet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjal, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel

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; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 20
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-20

Query Match      21.9%; Score 111; DB 15; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KRCINQLCKLPTDSELAPRS 21
DB 279 KRCINQLCKLPTDSELAPRS 299

RESULT 9
US-10-437-963-126312
; Sequence 126312, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 126312
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(131)
; OTHER INFORMATION: unsure at all Xaa locations
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_28871C.1.pep
US-10-437-963-126312

Query Match      16.0%; Score 81; DB 16; Length 131;
Best Local Similarity 25.9%; Pred. No. 0.15;
Matches 22; Conservative 12; Mismatches 41; Indels 10; Gaps 3;

OY 7 LLCKLPTDSELAPRSXCHCRHLIF-----EKTGSAITXCKENLPSLCSX---QGLRA 57
DB 8 LLCSSFD-DYSPRCRCHCRLVLCSTCQDSYKDYVCELCKQKNGKCCOTSPRQCKT 66

OY 58 BENITESCQXRLPPAAXOISOOLIP 82
DB 67 ESELIDSSDFGIPMIINKSATSTIP 91

RESULT 10
US-10-087-192-1977
; Sequence 1977, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1977
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-1977

Query Match      14.3%; Score 72.5; DB 13; Length 792;
Best Local Similarity 25.9%; Pred. No. 12;
Matches 28; Conservative 13; Mismatches 42; Indels 25; Gaps 5;

OY 7 LLCKLP-----TDSELAPR--SKCCHCRHLIFEKTSALTCKENLPSLCSXQGLRA 57
DB 204 IMCKWAPMVGKDITERLILPRFCWCCDCRMFVRKV-----CAANFGDICSVWGQA 256

OY 58 BENITESCQXRLPPAAXOISOOLIPTEASASXR---XKNQAKKXEPS 102
DB 257 TEML-----VRQAFQSLGPFISTTANPSSSGQCFKDESKNEDSS 298

RESULT 11
US-09-864-761-35896
; Sequence 35896, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
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;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/006666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 35896
;; LENGTH: 128
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL034431.13
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.99
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
;; OTHER INFORMATION: SWISSPROT HIT: P45559, EVALUATION 3.50e+00
;; OTHER INFORMATION: EST_HUMAN HIT: BF129465.1, EVALUATION 3.70e-01
US-09-864-761-35896

Query Match 13.6%; Score 69; DB 9; Length 128;
Best Local Similarity 26.2%; Pred. No. 3.7;
Matches 17; Conservative 10; Mismatches 18; Indels 20; Gaps 2;
Qy 21 SXCHCHLIFETKSAITXQCKENLPSLCSXQGLRAENITSCQXRLPPAAQISQOL 80
Db 22 SVCCCHYHIGTLGTVT-----VQGITATETLCKPCNLKFP-----QL 61
Qy 81 IPTEA 85
Db 62 LPLKS 66

RESULT 12
US-09-852-209A-13
; Sequence 13, Application US/09852209A
; Patent No. US20020164687A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin

;; APPLICANT: LEE, Xuri
;; APPLICANT: PONTEN, Annica
;; APPLICANT: UTELLA, Marko
;; APPLICANT: ALITALO, Kari
;; APPLICANT: OESTMAN, Arne
;; APPLICANT: HELDIN, Carl-Henrik
;; APPLICANT: BETSHOLTZ, Christer
;; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
;; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
;; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
;; CURRENT APPLICATION NUMBER: US/09/852,209A
;; CURRENT FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: 09/410,349
;; PRIOR FILING DATE: 1999-09-30
;; PRIOR APPLICATION NUMBER: 60/110,749
;; PRIOR FILING DATE: 1998-12-03
;; PRIOR APPLICATION NUMBER: 60/113,002
;; PRIOR FILING DATE: 1998-12-18
;; PRIOR APPLICATION NUMBER: 60/135,426
;; PRIOR FILING DATE: 1999-05-21
;; PRIOR APPLICATION NUMBER: 60/144,022
;; PRIOR FILING DATE: 1999-07-15
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 13
;; LENGTH: 358
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-852-209A-13

Query Match 13.5%; Score 68.5; DB 9; Length 358;
Best Local Similarity 27.5%; Pred. No. 14;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;
Qy 2 RCINQLLCKLPTDSELAPRSXCCHCHLIFETKSAITXQCKENLPSLCSXQGLRAENI 61
Db 273 RC--ECVCKAPCGDLIQHPENCSC-----FECKESLESQCKHKIHPD-- 315

Qy 62 TESCOXRLP 70
Db 316 TCSCEDRCP 324

RESULT 13
US-09-847-524-2
; Sequence 2, Application US/09847524
; Publication No. US20030166523A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G
; APPLICANT: STACKER, Steven A
; TITLE OF INVENTION: A METHOD FOR ACTIVATING ONLY THE VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR RECEPTOR-3 AND USES THEREOF
; FILE REFERENCE: Achen&Stacker-mouse VEPG-D
; CURRENT APPLICATION NUMBER: US/09/847,524
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-847-524-2

Query Match 13.5%; Score 68.5; DB 10; Length 358;
Best Local Similarity 27.5%; Pred. No. 14;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;
Qy 2 RCINQLLCKLPTDSELAPRSXCCHCHLIFETKSAITXQCKENLPSLCSXQGLRAENI 61
Db 273 RC--ECVCKAPCGDLIQHPENCSC-----FECKESLESQCKHKIHPD-- 315
Qy 62 TESCOXRLP 70

```
Db      316 TCSCEDRCP 324

RESULT 14
US-10-139-876-2
; Sequence 2, Application US/10139876
; Publication No. US20020123481A1
; GENERAL INFORMATION:
; APPLICANT: Oliviero, Salvatore
; TITLE OF INVENTION: C-Fos Induced Growth Factor (Fig) And Dna Encoding Same
; FILE REFERENCE: 35784/205172
; CURRENT APPLICATION NUMBER: US/10/139,876
; CURRENT FILING DATE: 2002-05-07
; PRIOR FILING DATE: 09/043,476
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: PCT/IB96/0113
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: GB9612368.2
; PRIOR FILING DATE: 1996-06-13
; PRIOR APPLICATION NUMBER: GB9519928.7
; PRIOR FILING DATE: 1995-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-139-876-2

Query Match      13.5%; Score 68.5; DB 13; Length 358;
Best Local Similarity 27.5%; Pred. No. 14;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;

Qy      2 RCINOLLCKLPTDSELAPRSXCCHRLIFEKTSAITXOCKENLPSCSXQGLFAEENI 61
Db      273 RC--ECVCKAPCPGDLIOHPENCSC-----FECKESLESCCQKHIFHPD-- 315

Qy      62 TESCOXRLP 70
Db      316 TCSCEDRCP 324

Search completed: April 15, 2005, 10:23:24
Job time : 132 secs

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-600-13

Query Match      13.5%; Score 68.5; DB 14; Length 358;
Best Local Similarity 27.5%; Pred. No. 14;
Matches 19; Conservative 8; Mismatches 25; Indels 17; Gaps 3;

Qy      2 RCINOLLCKLPTDSELAPRSXCCHRLIFEKTSAITXOCKENLPSCSXQGLFAEENI 61
Db      273 RC--ECVCKAPCPGDLIOHPENCSC-----FECKESLESCCQKHIFHPD-- 315

Qy      62 TESCOXRLP 70
Db      316 TCSCEDRCP 324

Search completed: April 15, 2005, 10:23:24
Job time : 132 secs

RESULT 15
US-10-131-600-13
; Sequence 13, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 10:20:35 ; Search time 44 Seconds
(without alignments)
225.235 Million cell updates/sec

Title: US-09-856-199-3

Perfect score: 103

Sequence: 1 KRCINQLCKLPTDSELAPR.....EASASXRKNQKXXEFSN 103

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	20.4	381	1 A47327	selenoprotein P pr
2	11	10.7	380	2 T10442	selenoprotein P pr
3	11	10.7	385	1 OMRTSP	selenoprotein P pr
4	7	6.8	258	2 AF2287	group 3 sigma 37-t
5	7	6.8	370	2 F84151	transcription regu
6	7	6.8	559	2 A25872	response regulator
7	7	6.8	1009	2 T47327	hypothetical prote
8	6	5.8	54	2 F82568	hypothetical prote
9	6	5.8	71	2 AC0673	conserved hypothet
10	6	5.8	75	2 B69326	hypothetical prote
11	6	5.8	85	2 G84331	hypothetical prote
12	6	5.8	92	2 E90889	hypothetical prote
13	6	5.8	92	2 D85728	hypothetical prote
14	6	5.8	93	2 T15339	hypothetical prote
15	6	5.8	129	2 D70026	hypothetical prote
16	6	5.8	133	2 C24925	lactose permease -
17	6	5.8	153	2 F95336	hypothetical prote
18	6	5.8	165	2 A71252	hypothetical prote
19	6	5.8	174	2 G83712	hypothetical prote
20	6	5.8	175	2 G69549	acetyl-CoA decarbo
21	6	5.8	178	2 F90020	50S ribosomal prot
22	6	5.8	180	1 RKWUAI	ribulose-bisphosph
23	6	5.8	180	2 G96694	hypothetical prote
24	6	5.8	186	2 S76419	probable ferredoxi
25	6	5.8	187	2 D83125	probable proteinase
26	6	5.8	191	2 D90040	hypothetical prote
27	6	5.8	194	2 A86017	hypothetical prote
28	6	5.8	194	2 A91171	hypothetical lipop
29	6	5.8	205	2 A71177	probable thymidyla

30	6	5.8	207	2 T36656	probable carbonic
31	6	5.8	208	2 T46927	hypothetical prote
32	6	5.8	210	2 F81386	probable acidic pe
33	6	5.8	217	2 A10870	hypothetical prote
34	6	5.8	221	2 S39522	hypothetical prote
35	6	5.8	222	2 S23731	MADS box protein T
36	6	5.8	228	2 T20219	hypothetical prote
37	6	5.8	236	2 E90674	hypothetical prote
38	6	5.8	236	2 H85524	hypothetical prote
39	6	5.8	248	2 G86387	hypothetical prote
40	6	5.8	249	2 A97227	polyferredoxin [im
41	6	5.8	255	1 S39737	glucose 1-dehydrog
42	6	5.8	259	2 B95267	probable ABC trans
43	6	5.8	272	2 H95954	probable Sir2-like
44	6	5.8	276	2 AG2532	hypothetical prote
45	6	5.8	280	2 S24720	ornithine carbamoy

ALIGNMENTS

RESULT 1

A47327
selenoprotein P precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: A47327; S42752
R: Hill, K.E.; Lloyd, R.S.; Burk, R.F.
Proc. Natl. Acad. Sci. U.S.A. 90, 537-541, 1993
A:Title: Conserved nucleotide sequences in the open reading frame and 3' untranslated re
A:Reference number: A47327; MUID:93133823; PMID:8421687
A:Accession: A47327
A:Molecule type: mRNA
A:Residues: 1-381 <HIL>
A:Cross-references: UNIPROT:P49908; GB:Z11793; NID:G36425; PIDN:CAA77836.1; PID:G2654365
A:Experimental source: heart and liver
A:Note: in Genbank entry HSEELPM, release 117.0, PIDN:CAA77836.1, the selenocysteine UCA
Biochim. Biophys. Acta 1204, 243-249, 1994
A:Title: Purification of selenoprotein P from human plasma.
A:Reference number: S42752; MUID:94191007; PMID:8142465
A:Accession: S42752
A:Molecule type: Protein
A:Residues: 20-27, 'X', 29-33 <AKE>
A:Note: mature forms of 55K and 61K were detected in plasma; the protein was shown to cor
C:Genetics:
A:Gene: GDB:SEPP1; SLNP
A:Cross-references: GDB:138278; OMIM:601484
A:Map position: 5q31-5q31
C:Function:
A:Description: may act as a free-radical scavenger
C:Superfamily: selenoprotein P
C:Keywords: extracellular protein; glycoprotein; heparin binding; liver; plasma; selenoc
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-381/Product: selenoprotein P #status experimental <MAT>
F:46.83,119,128,338/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:59,300,318,330,345,352,367,369,376,378/Modified site: selenocysteine #status predicted

Query Match 20.4%; Score 21; DB 1; Length 381;

Best Local Similarity 100.0%; Pred. No. 9.8e-15; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0;

Qy 1 KRCINQLCKLPTDSELAPRS 21
|||||

Db 279 KRCINQLCKLPTDSELAPRS 299
|||||

RESULT 2

T10442

selenoprotein P precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T10442

R;Steinert, P.; Ahrens, M.; Gross, G.; Flohe, L.
Biofactors 6, 311-319, 1997
A>Title: cDNA and deduced polypeptide sequence of a mouse selenoprotein P.
A:Reference number: Z17017; MUID:97434516; PMID:9288402
A:Accession: T10442
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-380 <STE>
A:Cross-references: EMBL:X99807; NID:g1495998; PIDN:CAA68140.1; PID:g1495999
C:Genetics:
A:Gene: selP
C:Superfamily: selenoprotein P
C:Keywords: extracellular protein; selenocysteine

Query Match 10.7%; Score 11; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CCHCRHLIFEK 33
| | | | | | | | | |
DB 301 CCHCRHLIFEK 311

RESULT 3
OMRTSP
C:Selenoprotein P precursor [validated] - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: A40380; B40380; S68322
R:Hill, K.E.; Lloyd, R.S.; Yang, J.G.; Read, R.; Burk, R.P.
J. Biol. Chem. 266, 10050-10053, 1991
A>Title: The cDNA for rat selenoprotein P contains 10 TGA codons in the open reading fra
A:Reference number: A40380; MUID:91244760; PMID:2037562
A:Accession: A40380
A:Molecule type: mRNA
A:Residues: 1-385 <HTL>
A:Cross-references: UNIPROT:P25236; GB:M63574; NID:g206893; PIDN:AAA42129.1; PID:g206894
A:Accession: B40380
A:Molecule type: protein
A:Residues: 20-41,267-287;316-327 <HI2>
R:Chittum, H.S.; Himeno, S.; Hill, K.E.; Burk, R.P.
Arch. Biochem. Biophys. 325, 124-128, 1996
A>Title: Multiple forms of selenoprotein P in rat plasma.
A:Reference number: S68322; MUID:96140605; PMID:8554336
A:Accession: S68322
A:Molecule type: protein
A:Residues: 20-27 <CHI>
C:Superfamily: selenoprotein P
C:Keywords: extracellular protein; glycoprotein; heparin binding; liver; plasma; seleno
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-385/Product: selenoprotein P #status experimental <MAT>
F:F59,264,335,357,371,373,380,382/Modified site: selenocysteine #status predicted
F:F83,174,198,370,375/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:F282,323/Modified site: selenocysteine #status experimental

Query Match 10.7%; Score 11; DB 1; Length 385;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CCHCRHLIFEK 33
| | | | | | | | | |
DB 306 CCHCRHLIFEK 316

RESULT 4
AF2287
group 3 sigma 37-type sigma factor [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF2287
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimono, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena dactyloides
A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AF2287

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-258 <KUR>

A;Cross-references: UNIPROT:Q8YQH5; GB:BA000019; PIDN:BAB75552.1; PID:g17132987; GSPDB:GN000001

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all3853

C;Superfamily: transcription sigma factor G; transcription initiation factor sigma katF 1

Query Match 6.8%; Score 7; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PTDSELA 18
| | | | |
DB 132 PTDSELA 138

RESULT 5

F84151

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans (strain ATCC 49041)
A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: F84151

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-370 <STO>

A;Cross-references: UNIPROT:Q9K5S4; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB0777

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH4014

C;Superfamily: response regulator aspartate phosphatase rapA

Query Match 6.8%; Score 7; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 KENLPSSL 49
| | | | |
DB 357 KENLPSSL 363

RESULT 6

A25872

A;Title: The sequence of the Saccharomyces cerevisiae gene PHO2 codes for a regulatory protein p1
A;Reference number: A25872; MUID:87146334; PMID:3029672

A;Accession: A25872

A;Molecule type: DNA

A;Residues: 1-559 <SEN>

A;Cross-references: UNIPROT:P07269; GB:M24613; NID:g4143; PIDN:CAA28729.1; PID:g4144

R;Ballesta, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, J.M.; Boles, L.

submitted to the Protein Sequence Database, July 1996

Nucleic Acids Res. 15, 233-246, 1987

A;Title: The sequence of the Saccharomyces cerevisiae gene PHO2 codes for a regulatory protein p1
A;Reference number: A25872; MUID:87146334; PMID:3029672

A;Accession: A25872

A;Molecule type: DNA

A;Residues: 1-559 <SEN>

A;Cross-references: UNIPROT:P07269; GB:M24613; NID:g4143; PIDN:CAA28729.1; PID:g4144

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A;Accession: A25872

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A;Residues: 1-559 <SEN>

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A;Accession: A25872

A;Molecule type: DNA

A;Residues: 1-559 <SEN>

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submitted to the Protein Sequence Database, July 1996

Nucleic Acids Res. 15, 233-246, 1987

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A;Reference number: A25872; MUID:87146334; PMID:3029672

A;Accession: A25872

A;Molecule type: DNA

A;Residues: 1-559 <SEN>

A;Cross-references: UNIPROT:P07269; GB:M24613; NID:g4143; PIDN:CAA28729.1; PID:g4144

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A;Accession: A25872

A;Molecule type: DNA

A;Residues: 1-559 <SEN>

A;Cross-references: UNIPROT:P07269; GB:M24613; NID:g4143; PIDN:CAA28729.1; PID:g4144

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A;Reference number: A25872; MUID:87146334; PMID:3029672

A;Accession: A25872

A;Molecule type: DNA

A;Residues: 1-559 <SEN>

A;Cross-references: UNIPROT:P07269; GB:M24613; NID:g4143; PIDN:CAA28729.1; PID:g4144

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A;Reference number: A25872; MUID:87146334; PMID:3029672

A;Accession: A25872

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A;Residues: 1-559 <SEN>

A;Cross-references: UNIPROT:P07269; GB:M24613; NID:g4143; PIDN:CAA28729.1; PID:g4144

R;Ballesta, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, J.M.; Boles, L.

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A;Title: The sequence of the Saccharomyces cerevisiae gene PHO2 codes for a regulatory protein p1
A;Reference number: A25872; MUID:87146334; PMID:3029672

A;Accession: A25872

A;Molecule type: DNA

A;Residues: 1-559 <SEN>

A;Cross-references: UNIPROT:P07269; GB:M24613; NID:g4143; PIDN:CAA28729.1; PID:g4144

R;Ballesta, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, J.M.; Boles, L.

submitted to the Protein Sequence Database, July 1996

Nucleic Acids

A:Experimental source: strain S288C
 R:McCarthy, B.J.; Creasy, C.L.; Bergman, L.W.
 Nucleic Acids Res. 19, 3463, 1991
 A:Title: Molecular analysis of a temperature sensitive allele of the PHO2 gene of *Saccharomyces cerevisiae*
 A:Reference number: S19636; MUID:91288241; PMID:2062666
 A:Accession: S19636
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 65-156, E', 158-310, N', 312-559 <MCC>
 A:Cross-references: EMBL:X54293; NID:G4146; PIDN:CAA38192.1; PID:G4147
 A:Experimental source: strain GG100-14D
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1990
 R:Bozkovic, J.; Saiz, J.E.; Soler-Mira, A.; Garcia-Cantalejo, J.; Revuelta, J.L.; Jimenez
 submitted to the EMBL Data Library, February 1996
 A:Reference number: S67406
 A:Accession: S67412
 A:Molecule type: DNA
 A:Residues: 1-559 <BOS>
 A:Cross-references: EMBL:X95644; NID:g1199535; PIDN:CAA64906.1; PID:e223187; PID:g119954
 R:Saiz, J.E.; Buitrago, M.J.; Garcia, R.; Revuelta, J.L.; del Rey, F.
 Yeast 12, 1077-1084, 1996
 A:Title: The sequence of a 20.3 kb DNA fragment from the left arm of *Saccharomyces cerevisiae*
 A:Reference number: S72094; MUID:97051597; PMID:8896274
 A:Accession: S72100
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-559 <SAI>
 A:Cross-references: EMBL:X95644; NID:g1199535; PIDN:CAA64906.1; PID:e223187; PID:g119954
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Genetics:
 A:Gene: SGD:GRF10; PHO2; BAS2
 A:Cross-references: MIPS:YDL106c; SGD:S0002264
 A:Map position: 4L
 C:Function:
 A:Description: required for expression of phosphate pathway and other genes; acts as a d
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:78-134/Domain: homeobox homology <HOX>

Query Match 6.8%; Score 7; DB 2; Length 559;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LPTDSEL 17
 |||||
 DB 533 LPTDSEL 539

RESULT 7
 T47327
 hypothetical protein T12K4.140 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C:Accession: T47327
 R:Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Rudd, S.; Lemcke, K.; May
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z24460
 A:Accession: T47327
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1009 <MON>
 A:Cross-references: UNIPROT:Q9M295; EMBL:AL138640
 A:Experimental source: cultivar Columbia; BAC clone T12K4
 C:Genetics:
 A:Map position: 3
 A:Introns: 130/2; 250/3; 567/3; 608/3; 638/3; 681/3; 782/2; 810/3
 A:Note: T12K4.140

Query Match 6.8%; Score 7; DB 2; Length 1009;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KLPTDSE 16

Db 82 KLPTDSE 88
 |||||
 RESULT 8
 F82568
 hypothetical protein XF2351 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: F82568
 R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: AB2515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: F82568
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-54 <SIM>
 A:Cross-references: UNIPROT:Q9PAZ4; GB:AE004045; GB:AE003849; NID:g9107517; PIDN:AAF8515
 R:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohne
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
 A:Authors: Martins, E.M.F.; Matukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF2351

Query Match 5.8%; Score 6; DB 2; Length 54;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 IPTAS 86
 |||||
 DB 13 IPTAS 18

RESULT 9
 AC0673
 conserved hypothetical protein STY1496 [imported] - Salmonella enterica subsp. enterica
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AC0673
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Cronin, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AC0673
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-71 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD01756.1; PID:g16502604; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY1496

Query Match 5.8%; Score 6; DB 2; Length 71;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 QGLRAE 58
 |||||
 Db 22 QGLRAE 27
 |||||

RESULT 10

B69326
 hypothetical protein AF0610 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: B69326
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: B69326
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-75 <LUE>
 A:Cross-references: UNIPROT:O29645; GB:AE001062; GB:AE000782; NID:G2689385; PIDN:AAB9063

Query Match 5.8%; Score 6; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 58 BENITE 63
 |||||
 Db 20 BENITE 25
 |||||

RESULT 11

G85431
 hypothetical protein AT4936570 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: G85431
 R:anonymous; The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: A85001; MUID:20083488; PMID:10617198
 A:Accession: G85431
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-85 <STO>
 A:Cross-references: UNIPROT:O23224; GB:NC_001268; NID:G7270605; PIDN:CAB80323.1; GSPDB:G
 C:Genetics:
 A:Gene: AT4936570
 A:Map position: 4

Query Match 5.8%; Score 6; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 57 AENIT 62
 |||||
 Db 47 AENIT 52
 |||||

RESULT 12

E90889
 hypothetical protein Ecs2085 [imported] - Escherichia coli (strain O157:H7, substrain RI
 C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C:Accession: E90889
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
 A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: E90889
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-92 <HAY>
 A:Cross-references: PIDN:BA35508.1; PID:g13361551; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RIND 050952
 C:Genetics:
 A:Gene: Ecs2085

Query Match 5.8%; Score 6; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 53 QGLRAE 58
 |||||
 Db 43 QGLRAE 48
 |||||

RESULT 13

DB5728
 hypothetical protein Z2229 [imported] - Escherichia coli (strain O157:H7, substrain EDL9)
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: DB5728
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: DB5728
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-92 <STO>
 A:Cross-references: GB:AE005174; NID:g12515200; PIDN:AAG56288.1; GSPDB:GN00145; UWGP:Z222
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Z2229

Query Match 5.8%; Score 6; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 53 QGLRAE 58
 |||||
 Db 43 QGLRAE 48
 |||||

RESULT 14

T15339
 hypothetical protein B0336.12 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T15339
 R:Taich, A.
 A:Description: The sequence of C. elegans cosmid B0336.
 A:Reference number: Z18331
 A:Accession: T15339
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-93 <TAI>
 A:Cross-references: UNIPROT:Q10957; EMBL:U32305; NID:g912752; PID:g912764; PIDN:AAC46838.
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:B0336.12
 A:Introns: 52/1; 64/1

Query Match 5.8%; Score 6; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 RHLIFE 32
 |||||

Db 35 RHLIFE 40

RESULT 15

D70026

hypothetical protein yuZE - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: D70026

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteaux, C.; Bron, S.; Broutlet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallez, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: D70026

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-129 <KUN>

A;Cross-references: UNIPROT:O32096; GB:Z99120; GB:AL009126; NID:G2635613; PIDN:CAB15169.

A;Experimental source: strain 168

C;Genetics:

A;Gene: yuZE

C;Supertfamily: Bacillus subtilis hypothetical protein yuZE

Query Match

Best Local Similarity 5.8%; Score 6; DB 2; Length 129;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

13 TDSELA 18

|||||

8 TDSELA 13

Db

Search completed: April 15, 2005, 10:30:20

Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 10:12:15 ; Search time 180 Seconds
(without alignments)
293.023 Million cell updates/sec

Title: US-09-856-199-3

Perfect score: 103

Sequence: 1 KRCINQLLCKLPTDSELA...BASASRXKQKQKXPSN 103

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	20.4	381	1	SELP_HUMAN	P49908 homo sapien
2	21	20.4	381	2	Q6PD59	Q6pd59 homo sapien
3	21	20.4	381	2	Q6PI43	Q6pi43 homo sapien
4	21	20.4	381	2	Q6PI87	Q6pi87 homo sapien
5	21	20.4	381	2	Q6PJF9	Q6pjf9 homo sapien
6	11	10.7	380	1	SELP_MOUSE	P70274 mus musculus
7	11	10.7	380	2	Q8OUF3	Q8ouf3 mus musculus
8	11	10.7	380	2	Q6PKE7	Q6pke7 mus musculus
9	11	10.7	385	1	SELP_RAT	P25236 rattus norv
10	9	8.7	380	2	Q8OT08	Q8ot08 mus musculus
11	9	8.7	386	2	Q8N2H6	Q8n2h6 bos taurus
12	9	8.7	402	1	SELP_BOVIN	P49907 bos taurus
13	8	7.8	383	2	Q6FDQ1	Q6fdq1 acinetobact
14	7	6.8	28	2	Q8E1T3	Q8e1t3 rabies viru
15	7	6.8	117	2	Q7SAM4	Q7sam4 neurospora
16	7	6.8	254	2	Q9V3M3	Q9v3m3 drosophila
17	7	6.8	258	2	Q8YQH5	Q8yqh5 anabaena sp
18	7	6.8	287	2	Q64WR6	Q64wr6 bacteroides
19	7	6.8	290	2	Q8JUL8	Q8jul8 lumpy skin
20	7	6.8	338	2	Q8TP43	Q8tp43 methanosarc
21	7	6.8	349	2	Q8RAG0	Q8rag0 thermoanaer
22	7	6.8	362	2	Q7VKB5	Q7vkb5 haemophilus
23	7	6.8	365	2	Q6SAS9	Q6sas9 sphingomona
24	7	6.8	370	2	Q9K5S4	Q9k5s4 bacillus ha
25	7	6.8	412	1	PGK_SPLIC	Q7wtu1 spiropasma
26	7	6.8	418	2	Q7NXP1	Q7npx1 chromobacte
27	7	6.8	431	2	Q7RZH7	Q7rzh7 neurospora
28	7	6.8	467	2	Q95FQ0	Q95fq0 malesherbia
29	7	6.8	477	2	Q95FN1	Q95fn1 paropsis ma
30	7	6.8	483	2	Q8MBF9	Q8mbf9 humbertia m
31	7	6.8	495	2	Q06858	Q06858 saccharomyc

32	7	6.8	555	2	Q7LBZ8	Q7lbz8 homo sapien
33	7	6.8	558	2	Q68CT6	Q68ct6 homo sapien
34	7	6.8	559	1	PHO2_YEAST	P07269 saccharomyc
35	7	6.8	569	2	Q9IMY7	Q9imy7 lumpy skin
36	7	6.8	570	2	Q9BUK6	Q9buk6 homo sapien
37	7	6.8	570	2	Q9NVU4	Q9nvu4 homo sapien
38	7	6.8	686	2	Q7QWU6	Q7qwv6 giardia lam
39	7	6.8	689	2	Q9VXW7	Q9vxw7 drosophila
40	7	6.8	704	2	Q7MIA4	Q7mia4 vibrio vuln
41	7	6.8	704	2	Q8DBL7	Q8dbl7 vibrio vuln
42	7	6.8	743	2	Q6C121	Q6c121 yarrowia li
43	7	6.8	839	2	Q98C24	Q98c24 rhizobium l
44	7	6.8	878	2	Q6GQK9	Q6gqk9 xenopus lae
45	7	6.8	932	1	CDG7_HUMAN	Q9y596 homo sapien

ALIGNMENTS

RESULT 1
SELP_HUMAN
ID SELP_HUMAN STANDARD; PRT; 381 AA.
AC P49908;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Selenoprotein P precursor (Sep).
GN Name=SEPP1; Synonyms=SELP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart, and Liver;
RX MEDLINE=93133823; PubMed=8421687;
RA Hill K.E., Lloyd R.S., Burk R.F.;
RT "Conserved nucleotide sequences in the open reading frame and 3'
RT untranslated region of selenoprotein P mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:537-541(1993).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=94191007; PubMed=8142465;
RA Aakesson B., Bellew T., Burk R.F.;
RT "Purification of selenoprotein P from human plasma.";
RL Biochim. Biophys. Acta 1204:243-249(1994).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98413836; PubMed=9735174; DOI=10.1006/abbi.1998.0809;
RA Mostert V., Lombeck I., Abel J.;
RT "A novel method for the purification of selenoprotein P from human
RT plasma.";
RL Arch. Biochem. Biophys. 357:326-330(1998).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=20239644; PubMed=10775431; DOI=10.1006/abbi.2000.1735;
RA Mostert V.;
RT "Selenoprotein P: properties, functions, and regulation.";
RL Arch. Biochem. Biophys. 376:433-438(2000).
RN [5]
RP REVIEW.
RX MEDLINE=95017128; PubMed=7931697;
RA Burk R.F., Hill K.E.;
RT "Selenoprotein P. A selenium-rich extracellular glycoprotein.";
RL J. Nutr. 124:1891-1897(1994).
CC -!- FUNCTION: Might be responsible for some of the extracellular
CC antioxidant defense properties of selenium or might be involved in
CC the transport of selenium. May supply selenium to tissues such as
CC brain and testis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Made in the liver and heart and secreted into
CC the plasma. It is also found in the kidney.
CC -!- MISCELLANEOUS: The selenocysteines are all encoded by the opal

```

CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; Z11793; CAA77836.1; -.
DR PIR; A47327; A47327.
DR Genew; HGNC:10751; SEPP1.
DR MIM; 601484; -.
DR GO; GO:0008430; F:selenium binding; TAS.
DR GO; GO:0006979; P:response to oxidative stress; TAS.
DR InterPro; IPR007672; Selp_C.
DR InterPro; IPR007671; Selp_N.
DR Pfam; PF04593; Selp_C; 1.
DR Pfam; PF04592; Selp_N; 1.
DR Direct protein sequencing; Glycoprotein; Plasma; Selenium;
KW Selenocysteine; Signal.
FT SIGNAL 1 19
FT CHAIN 20 381 Selenoprotein P.
FT DOMAIN 244 249 Poly-His.
FT SE_CYS 59 59
FT SE_CYS 300 300
FT SE_CYS 318 318
FT SE_CYS 330 330
FT SE_CYS 345 345
FT SE_CYS 352 352
FT SE_CYS 367 367
FT SE_CYS 369 369
FT SE_CYS 376 376
FT SE_CYS 378 378
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 83 83 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 119 119 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 128 128 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 174 174 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 338 338 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 381 AA; 42705 MW; 1A82FFA0BCD13CD7 CRC64;

Query Match 20.4%; Score 21; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLLCKLPTDSELAPRS 21
Db 279 KRCINQLLCKLPTDSELAPRS 299

RESULT 2
Q6PD59 PRELIMINARY; PRT; 381 AA.
AC Q6PD59
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
DE Selenoprotein P.
GN Name=SEPP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow, and Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RN Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RP [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC058919; AAH58919.1; -.
EMBL; BC005244; AAH05244.1; -.
DR GO; GO:0008430; F:selenium binding; IEA.
DR InterPro; IPR007672; Selp_C.
DR InterPro; IPR007671; Selp_N.
DR Pfam; PF04593; Selp_C; 1.
DR Pfam; PF04592; Selp_N; 1.
KW Selenium; Selenocysteine.
FT SE_CYS 59 59
FT SE_CYS 300 300
FT SE_CYS 318 318
FT SE_CYS 330 330
FT SE_CYS 345 345
FT SE_CYS 352 352
FT SE_CYS 367 367
FT SE_CYS 369 369
FT SE_CYS 376 376
FT SE_CYS 378 378
SQ SEQUENCE 381 AA; 42734 MW; 7A00BE7762D90833 CRC64;

Query Match 20.4%; Score 21; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLLCKLPTDSELAPRS 21
Db 279 KRCINQLLCKLPTDSELAPRS 299

RESULT 3
Q6PI43 PRELIMINARY; PRT; 381 AA.
AC Q6PI43
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Selenoprotein P.
GN Name=SEPP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
 RA Kryzinski M.I., Stalska U., Smalhus D.B., Schnerch A., Schein J.E.,
 RA Jones S.J., Maier M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015875; AAH15875.1; -;
 DR GO; GO:0008430; F:selenium binding; IEA.
 DR InterPro; IPR007672; Selp_C.
 DR InterPro; IPR007671; Selp_N.
 DR Pfam; PF04593; Selp_C; 1.
 DR Pfam; PF04592; Selp_N; 1.
 KW Selenium; Selenocysteine.
 DR SE_CYS 300 300
 FT SE_CYS 318 318
 FT SE_CYS 330 330
 FT SE_CYS 345 345
 FT SE_CYS 352 352
 FT SE_CYS 367 367
 FT SE_CYS 369 369
 FT SE_CYS 376 376
 FT SE_CYS 378 378
 FT SE_CYS 59 59
 SQ SEQUENCE 381 AA; 42705 MW; 4C195CA317ACBAID CRC64;

 Query Match 20.4%; Score 21; DB 2; Length 381;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 KRCINQLCKLPTDSELAPRS 21
 Db 279 KRCINQLCKLPTDSELAPRS 299

 RESULT 6
 ID SELP MOUSE STANDARD; PRT; 380 AA.
 AC P70274; Q32277;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Selenoprotein P precursor (Sep) (Plasma selenoprotein P).
 GN Name=Seppl; Synonyms=Selp;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RA Steinert P., Flohe L.;
 RT "Genomic DNA coding for mouse selenoprotein P.";
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RC -!- FUNCTION: Might be responsible for some of the extracellular

CC antioxidant defense properties of selenium or might be involved in
 CC the transport of selenium (By similarity). May supply selenium to
 CC tissues such as brain and testis.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -!- MISCELLANEOUS: The selenocysteines are all encoded by the opal
 CC codon, UGA.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X99807; CAA68140.1; -;
 CC EMBL; AF021345; AAD01684.1; -;
 CC MGD; MGI:894288; Seppl.
 CC InterPro; IPR007672; Selp_C.
 CC InterPro; IPR007671; Selp_N.
 CC Pfam; PF04593; Selp_C; 1.
 CC Pfam; PF04592; Selp_N; 1.
 KW Glycoprotein; Plasma; Selenium; Selenocysteine; Signal.
 DR SIGNAL 1 19
 FT CHAIN 20 380
 FT SE_CYS 59 59
 FT SE_CYS 259 259
 FT SE_CYS 277 277
 FT SE_CYS 318 318
 FT SE_CYS 330 330
 FT SE_CYS 352 352
 FT SE_CYS 366 366
 FT SE_CYS 368 368
 FT SE_CYS 375 375
 FT SE_CYS 377 377
 FT CARBOHYD 83 83
 FT CARBOHYD 176 176
 FT CARBOHYD 195 195
 FT CARBOHYD 365 365
 FT CARBOHYD 370 370
 FT CONFLICT 188 188
 FT CONFLICT 192 192
 FT CONFLICT 203 203
 SQ SEQUENCE 380 AA; 42236 MW; 72F7031941F47212 CRC64;

 Query Match 10.7%; Score 11; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 0.0057;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 23 CCHCRHLIFEK 33
 Db 301 CCHCRHLIFEK 311

 RESULT 7
 ID Q80UF3 PRELIMINARY; PRT; 380 AA.
 AC Q80UF3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus adult male kidney cDNA, RIKEN full-length enriched
 DE library, clone:0610010C08 product:selenoprotein P, plasma, 1, full
 DE insert sequence.
 GN Name=Seppl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RC SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RL 60,770 full-length cDNAs.";
RN Nature 420:563-573(2002).
RN [4]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RN Genome Res. 10:1617-1630(2000).
RN [5]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
RN [6]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RX EMBL; AK002450; BAC55246.2; --
DR MGD; MGI:894288; Seppl.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008430; F:selenium binding; IDA.
DR GO; GO:0007420; P:brain development; IMP.
DR GO; GO:0040007; P:growth; IMP.
DR GO; GO:0007626; P:locomotory behavior; IMP.
DR GO; GO:0009791; P:post-embryonic development; IMP.
DR GO; GO:0001887; P:selenium metabolism; IDA.
DR GO; GO:0019553; P:sexual reproduction; IMP.
DR InterPro; IPR007672; Sep C.
DR DR InterPro; IPR007671; Sep N.
DR Pfam; PF04593; Sep C; 1.
DR Pfam; PF04592; Sep N; 1.
DR Selenium; Selenocysteine.
FT SE_CYS 259

FT SE_CYS 277
FT SE_CYS 318
FT SE_CYS 321
FT SE_CYS 330
FT SE_CYS 332
FT SE_CYS 352
FT SE_CYS 366
FT SE_CYS 368
FT SE_CYS 375
FT SE_CYS 377
FT SE_CYS 59
SQ SEQUENCE 380 AA; 42268 MW; 72F7031B43F47010 CRC64;
Query Match 10.7%; Score 11; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CCHCRHLIFEK 33
Db 301 CCHCRHLIFEK 311
RESULT 8
Q6PK67 PRELIMINARY; PRT; 380 AA.
AC Q6PK67;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Selenoprotein P, plasma, 1.
GN Name=Seppl;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001991; AA01991.2; --
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008430; F:selenium binding; IDA.
DR GO; GO:0007420; P:brain development; IMP.
DR GO; GO:0040007; P:growth; IMP.
DR GO; GO:0007626; P:locomotory behavior; IMP.
DR GO; GO:0009791; P:post-embryonic development; IMP.
DR GO; GO:0001887; P:selenium metabolism; IDA.
DR GO; GO:0019553; P:sexual reproduction; IMP.
DR InterPro; IPR007672; Sep C.
DR InterPro; IPR007671; Sep N.

```

DR InterPro; IPR007671; Selp_N.
DR Pfam; PF04593; Selp_C; 1.
DR KJ; PF04592; Selp_N; 1.
KW Selenium; Selenocysteine.
FT SE_CYS 259 259
FT SE_CYS 277 277
FT SE_CYS 318 318
FT SE_CYS 321 321
FT SE_CYS 330 330
FT SE_CYS 352 352
FT SE_CYS 366 366
FT SE_CYS 368 368
FT SE_CYS 375 375
FT SE_CYS 377 377
FT SE_CYS 59 59
SQ SEQUENCE 380 AA; 42281 MW; F9F0EA15B8F39005 CRC64;

Query Match 10.7%; Score 11; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CCHCRHLIFEK 33
DB 301 CCHCRHLIFEK 311

RESULT 9
SELP_RAT STANDARD; PRT; 385 AA.
AC P25236;
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Selenoprotein P precursor (Sep).
GN Name=Seppl; Synonyms=Selp;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-41; 267-287 AND 316-327.
RC TISSUE=Liver;
RX MEDLINE=91244760; PubMed=2037562;
RA Hill K.E., Lloyd R.S., Yang J.-G., Read R., Burk R.F.;
RT "The cDNA for rat selenoprotein P contains 10 TGA codons in the open
RL reading frame.";
RL J. Biol. Chem. 266:10050-10053 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=95364621; PubMed=7637580; DOI=10.1016/0169-328X(94)00007-2;
RA Saijoh K., Saito N., Lee M.J., Fujii M., Kobayashi T., Sumino K.;
RT "Molecular cloning of cDNA encoding a bovine selenoprotein P-like
RT protein containing 12 selenocysteines and a (His-Pro) rich domain
RL insertion, and its regional expression.";
RL Brain Res. Mol. Brain Res. 30:301-311 (1995).
RN [3]
RP CHARACTERIZATION OF ISOFORMS.
RX PubMed=11821412; DOI=10.1074/jbc.M111462200;
RA Ma S., Hill K.E., Caprioli R.M., Burk R.F.;
RT "Mass spectrometric characterization of full-length rat selenoprotein
RT P and three isoforms shortened at the C terminus. Evidence that three
RT UGA codons in the mRNA open reading frame have alternative functions
RL of specifying selenocysteine insertion or translation termination.";
RL J. Biol. Chem. 277:12749-12754 (2002).
RN [4]
RP CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX PubMed=12911312; DOI=10.1021/bi0346300;
RA Ma S., Hill K.E., Burk R.F., Caprioli R.M.;
RT "Mass spectrometric identification of N- and O-glycosylation sites of
RT full-length rat selenoprotein P and determination of selenide-sulfide
RT and disulfide linkages in the shortest isoform.";
RL Biochemistry 42:9703-9711 (2003).

(5)
RN REVIEW.
RX MEDLINE=95017128; PubMed=7931697;
RA Burk R.F., Hill K.E.;
RT "Selenoprotein P, A selenium-rich extracellular glycoprotein.";
RL J. Nutr. 124:1891-1897 (1994).
CC -!- FUNCTION: Might be responsible for some of the extracellular
CC antioxidant defense properties of selenium or might be involved in
CC the transport of selenium. May supply selenium to tissues such as
CC brain and testis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Widely expressed, mainly by the liver.
CC Secreted in plasma.
CC -!- PTM: Isoform Se-P1 contains several disulfide bridges and a
CC selenide-sulfide bond between Sec-59 and Cys-62. These bonds are
CC -!- MISCELLANEOUS: Plasma contains 4 isoforms, which are named
CC isoforms Se-P10, Se-P6, Se-P2 and Se-P1, according to the number
CC of selenocysteines they contain. All isoforms arise from the same
CC mRNA. The 3 shortened isoforms terminated at the opal STOP codons
CC at positions 264, 282, 371, when selenocysteine has not been
CC inserted.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M63574; AAA42129.2; -
CC EMBL; D25221; BAA04950.2; -
CC PIR; A40380; OMRTPS.
CC RGD; 3660; Seppl.
CC InterPro; IPR007672; Selp_C.
CC InterPro; IPR007671; Selp_N.
CC Pfam; PF04593; Selp_C; 1.
CC Pfam; PF04592; Selp_N; 1.
CC Direct protein sequencing; Glycoprotein; Plasma; Selenium;
KW Selenocysteine; Signal.
FT SIGNAL 1 19
FT CHAIN 20 263 Selenoprotein P, isoform Se-P1.
FT CHAIN 20 281 Selenoprotein P, isoform Se-P2.
FT CHAIN 20 370 Selenoprotein P, isoform Se-P6.
FT CHAIN 20 385 Selenoprotein P, isoform Se-P10.
FT DOMAIN 244 252 Poly-His.
FT CROSSLNK 59 62 CysteinyI-selenocysteine (Sec-Cys) (in
FT isoform Se-P1).
FT DISULFID 168 186 In isoform Se-P1.
FT DISULFID 172 175 In isoform Se-P1.
FT SE_CYS 59 59
FT SE_CYS 264 264
FT SE_CYS 282 282
FT SE_CYS 323 323
FT SE_CYS 335 335
FT SE_CYS 357 357
FT SE_CYS 371 371
FT SE_CYS 373 373
FT SE_CYS 380 380
FT SE_CYS 382 382
FT CARBOHYD 83 83 N-linked (GlcNAc...).
FT CARBOHYD 174 174 N-linked (GlcNAc...).
FT CARBOHYD 188 188 N-linked (Hex...); partial.
FT CARBOHYD 365 365 O-linked (Hex...); partial.
SQ SEQUENCE 385 AA; 42614 MW; 013BDF4FB741E3B8 CRC64;

Query Match 10.7%; Score 11; DB 1; Length 385;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CCHCRHLIFEK 33
|||||

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Db 306 CCHCRHLIFEK 316

RESULT 10

Q80T08 PRELIMINARY; PRT; 380 AA.

AC Q80T08;

DT 01-JUN-2003 (TRENBLrel. 24, Created)

DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,

DE RIKEN full-length enriched library, clone:5031434C21

DE product:selenoprotein P, plasma, 1, full insert sequence.

GN Name=Seppl;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

XP [1]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;

RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;

RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;

RA The FANTOM Consortium;

RA The RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;

RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [5]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;

RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;

RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,

RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoaka T., Hori F.,

RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura R., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai K.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,

RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK077265; BAC55264.2; -

DR MGD; MGI:894288; Seppl.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0008430; P:selenium binding; IDA.

DR GO; GO:0007420; P:brain development; IMP.

DR GO; GO:0040007; P:growth; IMP.

DR GO; GO:0007626; P:locomotory behavior; IMP.

DR GO; GO:0009791; P:post-embryonic development; IMP.

DR GO; GO:0010887; P:selenium metabolism; IDA.

DR GO; GO:0019953; P:sexual reproduction; IMP.

DR InterPro; IPR007671; Selp_C.

DR Pfam; PF04593; Selp_C; 1.

DR Pfam; PF04592; Selp_N; 1.

KW Selenium; Selenocysteine.

FT SE_CYS 259 259

FT SE_CYS 277 277

FT SE_CYS 318 318

FT SE_CYS 330 330

FT SE_CYS 352 352

FT SE_CYS 366 366

FT SE_CYS 372 372

FT SE_CYS 375 375

FT SE_CYS 377 377

FT SE_CYS 59 59

SQ SEQUENCE 380 AA; 42272 MW; 4D1EB91BD89F89D1 CRC64;

Query Match 8.7%; Score 9; DB 2; Length 380;

Best Local Similarity 100.0%; Pred. No. 0.76;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 CINQLLCKL 11

Db 281 CINQLLCKL 289

RESULT 11

Q9N2H6 PRELIMINARY; PRT; 386 AA.

AC Q9N2H6;

DT 01-OCT-2000 (TRENBLrel. 15, Created)

DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE Selenoprotein P.

GN Name=selp;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.

OX NCBI_TaxID=9913;

XP [1]

SEQUENCE FROM N.A.

RA Hara S., Imura N., Shoji Y.;

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB032826; BAA84781.1; -

DR GO; GO:0008430; P:selenium binding; IEA.

DR InterPro; IPR007672; Selp_C.

DR InterPro; IPR007671; Selp_N.

DR Pfam; PF04593; Selp_C; 1.

DR Pfam; PF04592; Selp_N; 1.

KW Selenium; Selenocysteine.

FT SE_CYS 281 281

FT SE_CYS 291 291

FT SE_CYS 322 322

FT SE_CYS 334 334

FT SE_CYS 347 347

FT SE_CYS 349 349

FT SE_CYS 356 372
 FT SE_CYS 372 372
 FT SE_CYS 374 374
 FT SE_CYS 381 381
 FT SE_CYS 383 383
 FT SE_CYS 59 59
 SQ SEQUENCE 386 AA; 43061 MW; ECGF3A76874E528F CRC64;

Query Match 8.7%; Score 9; DB 2; Length 386;
 Best Local Similarity 100.0%; Pred. No. 0.77;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINQLLC 9
 |||||
 Db 283 KRCINQLLC 291

RESULT 12

SELP_BOVIN STANDARD; PRT; 402 AA.
 AC P49507; O19003;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Selenoprotein P-like protein precursor.
 OS Name=SEPP1; Synonyms=SELP;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum.
 RX MEDLINE=95364621; PubMed=7637590; DOI=10.1016/0169-328X(94)00007-2;
 RA Sajoh K., Saito M., Lee M.J., Fujii M., Kobayashi T., Sumino K.;
 RT "Molecular cloning of cDNA encoding a bovine selenoprotein P-like
 protein containing 12 selenocysteines and a (His-Pro) rich domain
 insertion, and its regional expression."
 RT Brain Res. Mol. Brain Res. 30:301-311(1995).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98019090; PubMed=9358058; DOI=10.1016/S0378-1119(97)00369-7;
 RA Fujii M., Sajoh K., Kobayashi T., Fujii S., Lee M.J., Sumino K.;
 RT "Analysis of bovine selenoprotein P-like protein gene and availability
 of metal responsive element (MRE) located in its promoter."
 RL Gene 199:211-217(1997).
 CC -!- FUNCTION: It constitutes a major selenium pool in the brain and
 may play an important role in developing and/or modulating the
 morphology of neurons and/or glial cells.
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- TISSUE SPECIFICITY: Brain and kidney. Most prominently expressed
 in the cerebellar cortex, hippocampus and olfactory bulb.
 CC -!- MISCELLANEOUS: the selenocysteines are all encoded by the opal
 codon, UGA.

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 or send an email to license@isb-sib.ch).

DR EMBL; D25220; BAA04949.2; -
 DR EMBL; D88033; BAA23414.1; -
 DR EMBL; D88031; BAA23414.1; JOINED.
 DR EMBL; D88032; BAA23414.1; JOINED.
 DR InterPro; IPR007672; SelP_C.
 DR InterPro; IPR007671; SelP_N.
 DR Pfam; PF04593; SelP_C; 1.
 DR Pfam; PF04592; SelP_N; 1.
 KW Glycoprotein; Repeat; Selenium; Selenocysteine; Signal.

FT SIGNAL 1 19
 FT CHAIN 20 402
 FT SE_CYS 59 59
 FT SE_CYS 297 297
 FT SE_CYS 307 307
 FT SE_CYS 338 338
 FT SE_CYS 350 350
 FT SE_CYS 363 363
 FT SE_CYS 365 365
 FT SE_CYS 372 372
 FT SE_CYS 388 388
 FT SE_CYS 390 390
 FT SE_CYS 397 397
 FT SE_CYS 399 399
 FT CARBOHYD 83 83
 FT CARBOHYD 174 174
 FT DOMAIN 204 229
 FT REPEAT 204 205
 FT REPEAT 206 207
 FT REPEAT 208 209
 FT REPEAT 210 211
 FT REPEAT 212 213
 FT REPEAT 214 215
 FT REPEAT 216 217
 FT REPEAT 218 219
 FT REPEAT 220 221
 FT REPEAT 222 223
 FT REPEAT 224 225
 FT REPEAT 226 227
 FT REPEAT 228 229
 FT DOMAIN 260 266
 FT CONFLICT 178 181
 FT CONFLICT 256 256
 FT CONFLICT 282 282
 FT CONFLICT 312 312
 SQ SEQUENCE 402 AA; 45018 MW; B7CF18751FB0E8FF CRC64;

By similarity.
 Selenoprotein P-like protein.
 N-linked (GlcNAc...) (By similarity).
 N-linked (GlcNAc...) (By similarity).
 13 X 2 AA tandem repeats of H-[PHS].
 1.
 2.
 3.
 4.
 5.
 6.
 7.
 8.
 9.
 10.
 11.
 12.
 13.
 SRPQ -> KALE (in Ref. 2).
 T -> P (in Ref. 2).
 L -> V (in Ref. 2).
 Y -> D (in Ref. 2).
 N-linked (GlcNAc...) (By similarity).
 N-linked (GlcNAc...) (By similarity).
 13 X 2 AA tandem repeats of H-[PHS].

Query Match 8.7%; Score 9; DB 1; Length 402;
 Best Local Similarity 100.0%; Pred. No. 0.79;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINQLLC 9
 |||||
 Db 299 KRCINQLLC 307

RESULT 13

Q6FDQ1 ID Q6FDQ1 PRELIMINARY; PRT; 383 AA.
 AC Q6FDQ1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Twitching motility protein.
 GN Name=pf10; OrderedLocustNames=ACIAD0911;
 OS Acinetobacter sp. (strain ADP1).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=62977;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barbe V., Vallonet D., Fonknechten N., Kreimeyer A., Oztas S.,
 RA Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,
 RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
 RT "Unique features revealed by the genome sequence of Acinetobacter sp.
 ADP1, a versatile and naturally transformation competent bacterium."
 RL Nucleic Acids Res. 0:0-0(2004).
 DR EMBL; CR543861; CAG67807.1; -
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_Arpase.

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DR InterPro; IPR001482; GSP11_E.
DR InterPro; IPR006321; P1LT.
DR Pfam; PF00437; GSP11_E; 1.
DR ProDom; PD000739; GSP11_E; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR01420; p1lt fam; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 383 AA; 43616 MW; 4D64965D121D383F CRC64;

Query Match 7.8%; Score 8; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 ISQOLIPT 83
Db 265 ISQOLIPT 272
|||||

RESULT 14
Q9E1T3 PRELIMINARY; PRT; 28 AA.
AC Q9E1T3
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE L protein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP SEQUENCE FROM N.A.
RA Pacz A., Duarte X., Pulido S.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF276906; AAG24801.1; -
FT NON TER 28
SQ SEQUENCE 28 AA; 2953 MW; 2E330EA9A88F3C6A CRC64;

Query Match 6.8%; Score 7; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 DSELAPR 20
Db 16 DSELAPR 22
|||||

RESULT 15
Q7SAM4 PRELIMINARY; PRT; 117 AA.
AC Q7SAM4
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Predicted protein (Hypothetical protein B2N18.150).
GN Name=NCU08017.1; Synonym=B2N18.150;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kanal M., Kamyselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kryzstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,

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RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Eboile D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX0100203; EAA33451.1; -.
DR EMBL; BX897674; CAE85516.1; -.
DR GO; GO:0004219; F:Pyroglutami-peptidase I activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000816; Peptidase_C15.
KW Hypothetical protein.
SQ SEQUENCE 117 AA; 12796 MW; A7DAE27D4E758697 CRC64;

Query Match 6.8%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 KENLPSL 49
Db 109 KENLPSL 115
|||||

Search completed: April 15, 2005, 10:29:30
Job time : 183 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 10:11:30 ; Search time 172 Seconds

(without alignments)
231.607 Million cell updates/sec

Title: US-09-856-199-3

Perfect score: 103

Sequence: 1 KRCINQLLCKLPTDSELA.....EASASXRXKXKXEXPSN 103

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	91.3	103	6	Abp71716 Human sel
2	94	91.3	103	6	Abp55510 Human pla
3	94	91.3	103	6	Abp57372 Selenopro
4	94	91.3	103	6	Abp99457 Amino aci
5	94	91.3	103	7	Adf53279 Human sel
6	94	91.3	103	8	Ado71758 Human sel
7	94	91.3	103	8	Adp90528 C-termina
8	94	91.3	362	8	Ado71757 Human sel
9	94	91.3	362	8	Adp90527 Human sel
10	94	91.3	381	5	Aau84306 Human end
11	94	91.3	381	6	Abu89753 Protein d
12	32	31.1	33	6	Abp55511 Human pla
13	32	31.1	33	6	Abp57373 Selenopro
14	32	31.1	33	6	Abp99458 Amino aci
15	32	31.1	33	8	Ado71759 Human sel
16	32	31.1	33	8	Adp90529 Human sel
17	29	28.2	30	7	Adf53280 Human sel
18	28	27.2	29	5	Aau97702 Human sel
19	28	27.2	29	6	Abp55508 Human pla
20	28	27.2	29	6	Abp99455 Amino aci
21	28	27.2	29	8	Ado71760 Human sel
22	28	27.2	29	8	Adp90530 Human sel
23	26	25.2	28	5	Aau97703 Human sel
24	26	25.2	28	6	Abp55509 Human pla
25	26	25.2	28	6	Abp99456 Amino aci

26	26	25.2	28	7	Adf53281 Human sel
27	26	25.2	28	8	Ado71761 Human sel
28	26	25.2	28	8	Adp90531 Human sel
29	21	20.4	21	3	AAb03187 Human neu
30	21	20.4	21	6	Abp71718 Human neu
31	21	20.4	21	6	Abp55512 Human pla
32	21	20.4	21	6	Abp57374 Selenopro
33	21	20.4	21	6	Abp99459 Amino aci
34	21	20.4	29	3	AAb03183 Human sel
35	21	20.4	103	3	AAb03185 Human sel
36	21	20.4	110	3	AAg03755 Human sec
37	21	20.4	240	3	AAb57080 Human pro
38	21	20.4	299	7	Ado40114 Human NOV
39	21	20.4	380	7	Adn95151 Human BEC
40	21	20.4	381	3	AAb03188 Human sel
41	21	20.4	381	7	Ado47226 Human pro
42	21	20.4	381	7	Adp65180 Human sel
43	20	19.4	20	3	AAb03186 Human sel
44	13	12.6	14	6	Abp71715 Human neu
45	13	12.6	14	6	Abp57371 Cytotoxic

ALIGNMENTS

RESULT 1

ABP71716

ID ABP71716 standard; peptide; 103 AA.

XX AC ABP71716;

DT 17-APR-2003 (first entry)

DE Human selenoprotein P C-terminal peptide fragment # SEQ ID 3.

KW Neurodegenerative disease; selenoprotein P; nootropic; neuroprotective; anticonvulsant; motor ataxia; Alzheimer's disease; senile dementia; Huntington's chorea; supranuclear paralysis; epilepsy; human; spinocerebellar degeneration.

XX OS Homo sapiens.

XX Key Location/Qualifiers.

FT Modified-site /label= OTHER

FT /note= "selenocysteine"

FT Modified-site /label= OTHER

FT /note= "selenocysteine"

FT Modified-site /label= OTHER

FT /note= "selenocysteine"

FT Modified-site /label= OTHER

FT /note= "selenocysteine"

FT Modified-site /label= OTHER

FT /note= "selenocysteine"

FT Modified-site /label= OTHER

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FT Modified-site /label= OTHER

FT /note= "selenocysteine"

FT Modified-site /label= OTHER

FT /note= "selenocysteine"

FT Modified-site /label= OTHER

FT WO200292121-A1.

XX 21-NOV-2002.

XX 10-MAY-2002; 2002WO-JP004558.

PF

XX PR 11-MAY-2001; 2001JP-00141462.
 XX PA (KAGA) CEMO-SERO-THERAPEUTIC RES INST.
 XX PA (HISM) HISAMITSU PHARM CO LTD.
 XX PI Hirashima M, Naruse T, Maeda H, Nozaki C, Goto T, Akiyama K;
 XX PI Fukushima H;
 XX DR WPI; 2003-156710/15.
 XX PT New remedies for neurodegenerative diseases showing motor ataxia as major
 XX PT symptom such as Alzheimer's disease, senile dementia, Huntington's chorea
 XX PT and supranuclear palsy, comprising selenoprotein P or its C-terminal
 XX PT peptide(s).
 XX PS Example 2; Page 9; 3lpp; Japanese.
 XX CC The invention relates to new remedies for neurodegenerative diseases
 XX CC comprising selenoprotein P, or its C-terminal peptide(s). The activity of
 XX CC peptides of the invention may be described as neurotropic, neuroprotective
 XX CC and anticonvulsant. The remedies are for neurodegenerative diseases
 XX CC showing motor ataxia as a major symptom. These include (juvenile)
 XX CC Alzheimer's disease, senile dementia, Huntington's chorea, supranuclear
 XX CC palsy, spinocerebellar degeneration and difficult-to-cure epilepsy.
 XX CC The current sequence represents the human selenoprotein P C-terminal
 XX CC peptide fragment
 XX PS Sequence 103 AA;
 CC Query Match 91.3%; Score 94; DB 6; Length 103;
 CC Best Local Similarity 100.0%; Pred. No. 1.8e-95;
 CC Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPTDSELAPRSXCHCHRLIFETKTSALTQCKENLPSLCSXQGLRAEN 60
 DB 1 KRCINQLLCKLPTDSELAPRSXCHCHRLIFETKTSALTQCKENLPSLCSXQGLRAEN 60
 QY 61 ITESQXRLPPAAXQISQQLIPTASASXRXKNOAKKXEPN 103
 DB 61 ITESQXRLPPAAXQISQQLIPTASASXRXKNOAKKXEPN 103
 RESULT 2
 ABP55510 standard; protein; 103 AA.
 AC ABP55510;
 DT 18-FEB-2003 (first entry)
 DE Human plasma selenoprotein P SEQ ID NO:3.
 KW Human; plasma; selenoprotein P; neurodegenerative disease;
 KW motor disorder; depression; neurotropic; neuroprotective; anticonvulsant;
 KW cerebroprotective; aging; traumatic cerebrovascular damage; epilepsy;
 KW motoneuron disease.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Modified-site 22 /note= "selenocysteine"
 FT Modified-site 40 /note= "selenocysteine"
 FT Modified-site 52 /note= "selenocysteine"
 FT Modified-site 67 /note= "selenocysteine"
 FT Modified-site 74 /note= "selenocysteine"
 FT Modified-site 89 /note= "selenocysteine"
 FT Modified-site /note= "selenocysteine"

FT Modified-site 91 /note= "selenocysteine"
 FT Modified-site 98 /note= "selenocysteine"
 FT Modified-site 100 /note= "selenocysteine"
 FT W0200276492-Al.
 XX FN 03-OCT-2002.
 XX 31-AUG-2001; 2001WO-JP007525.
 XX 23-MAR-2001; 2001JP-00084050.
 XX (KAGA) CEMO-SERO-THERAPEUTIC RES INST.
 XX Hirashima M, Sasaki T, Naruse T, Maeda H, Nozaki C;
 XX WPI; 2003-059349/05.
 CC Selenoprotein P-based novel remedies for ameliorating neurodegenerative
 CC diseases e.g. motor disorders including diseases associated with
 CC depression of motor function e.g. ageing, traumatic cerebrovascular
 CC damage and epilepsy.
 CC PS Disclosure; Page 8; 27pp; Japanese.
 CC The present invention describes agents (I) for ameliorating motor
 CC disorders, containing as the main component selenoprotein P and/or its C-
 CC terminal peptides. (I) have neurotropic, neuroprotective cerebroprotective
 CC and anticonvulsant activities. (I) can be used for ameliorating
 CC neurodegenerative diseases e.g. motor disorders including diseases
 CC associated with depression of motor function e.g. aging, traumatic
 CC cerebrovascular damage, epilepsy, motoneuron disease. The present
 CC sequence represents the human plasma selenoprotein P protein which is
 CC used in the present invention
 XX Sequence 103 AA;
 CC Query Match 91.3%; Score 94; DB 6; Length 103;
 CC Best Local Similarity 100.0%; Pred. No. 1.8e-95;
 CC Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPTDSELAPRSXCHCHRLIFETKTSALTQCKENLPSLCSXQGLRAEN 60
 DB 1 KRCINQLLCKLPTDSELAPRSXCHCHRLIFETKTSALTQCKENLPSLCSXQGLRAEN 60
 QY 61 ITESQXRLPPAAXQISQQLIPTASASXRXKNOAKKXEPN 103
 DB 61 ITESQXRLPPAAXQISQQLIPTASASXRXKNOAKKXEPN 103
 RESULT 3
 ABP57372 standard; protein; 103 AA.
 AC ABP57372;
 DT 23-APR-2003 (first entry)
 DE Selenoprotein P fragment SEQ ID NO:2.
 KW Cytotoxicity inhibitor; selenocysteine; selenoprotein P; human; plasma;
 KW neurotropic; neuroprotective; antiarteriosclerotic; anti-HIV; AIDS;
 KW Alzheimer's disease; arteriosclerosis; cosmetic.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Modified-site 22 /note= "selenocysteine"
 FT Modified-site 40 /note= "selenocysteine"

FT Modified-site /note= "selenocysteine"
 FT Modified-site /note= "selenocysteine"
 FT Modified-site /note= "selenocysteine"
 FT Modified-site /note= "selenocysteine"
 FT Modified-site /note= "selenocysteine"
 FT Modified-site /note= "selenocysteine"
 FT Modified-site /note= "selenocysteine"
 FT Modified-site /note= "selenocysteine"
 FT Modified-site /note= "selenocysteine"

WO200292810-A1.

21-NOV-2002.

10-MAY-2002; 2002WO-JP004557.

11-MAY-2001; 2001JP-00141466.

(KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
 (HISM) HISAMITSU PHARM CO LTD.

Hirashima M, Naruse T, Maeda H, Nozaki C, Goto T, Akiyama K;
 Hattori W;

WPI; 2003-129291/12.

Screening of functional peptides with lower cytotoxicity than
 selenocysteine and cytotoxicity inhibitory activity, for use in drugs for
 diseases like Alzheimer's disease, AIDS and arteriosclerosis, and in
 cosmetics.

Example 1; Page 15; 43pp; Japanese.

The present invention describes peptides (I) comprising one or more
 selenocysteines that show lower cytotoxicity than selenocysteine and
 cytotoxicity inhibitory activity. Also described is a method for
 screening substances with cytotoxicity inhibitory activity by using the
 sudden cell death phenomenon in a cell culture system with an albumin or
 fatty acid-added serum-free medium for culturing a test substance, and
 evaluating the degree of cytotoxicity based on generation of peroxidised
 lipid, or glutathione peroxidase activity, as indication. (I) have
 neurotropic, neuroprotective, antiarteriosclerotic and anti-HIV activities.
 The screened peptides are useful for drugs for diseases like Alzheimer's
 disease, AIDS and arteriosclerosis, and in cosmetics. The present
 sequence represents a selenoprotein P fragment, which is used in an
 example from the present invention

Sequence 103 AA;

Query Match 91.3%; Score 94; DB 6; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.8e-95;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINQLLCKLPTDSELAPRSXCCHRLIFKGTSAITXCKENLPISLCSXQGLRAEN 60
 DB 1 KRCINQLLCKLPTDSELAPRSXCCHRLIFKGTSAITXCKENLPISLCSXQGLRAEN 60
 QY 61 ITESCQXRLPPAAXQISQOLIPTTEASASRXKXNQAKXEXPSN 103
 DB 61 ITESCQXRLPPAAXQISQOLIPTTEASASRXKXNQAKXEXPSN 103

RESULT 4

ABB99457

ID ABB99457 standard; peptide; 103 AA.

XX

AC ABB99457;

XX 12-FEB-2003 (first entry)

XX Amino acid sequence of a peptide derived from human selenoprotein P.
 XX Selenoprotein P; immunopathic disease; autoimmune disease;
 XX rheumatoid arthritis; multiple sclerosis; allergic disease;
 XX bronchial asthma.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Modified-site 22 /note= "selenocysteine"
 FT Modified-site 40 /note= "selenocysteine"
 FT Modified-site 52 /note= "selenocysteine"
 FT Modified-site 67 /note= "selenocysteine"
 FT Modified-site 74 /note= "selenocysteine"
 FT Modified-site 89 /note= "selenocysteine"
 FT Modified-site 91 /note= "selenocysteine"
 FT Modified-site 98 /note= "selenocysteine"
 FT Modified-site 100 /note= "selenocysteine"
 FT Modified-site /note= "selenocysteine"

WO200276493-A1.

03-OCT-2002.

20-MAR-2002; 2002WO-JP002645.

23-MAR-2001; 2001JP-00084049.

(KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

Hirashima M, Sasaki T, Naruse T, Maeda H, Nozaki C;

WPI; 2003-058350/05.

Selenoprotein P-derived novel drugs for preventing or treating
 immunopathic diseases including autoimmune diseases like rheumatoid
 arthritis and multiple sclerosis, and allergic diseases e.g. bronchial
 asthma.

Disclosure; Page 7; 26pp; Japanese.

XX The present sequence represents a C-terminal peptide of selenoprotein P.
 CC The peptide is used in drugs for preventing/treating immunopathic
 CC diseases. The drugs are used for preventing or treating immunopathic
 CC diseases including autoimmune diseases like rheumatoid arthritis and
 CC multiple sclerosis, and allergic diseases e.g. bronchial asthma

Sequence 103 AA;

Query Match 91.3%; Score 94; DB 6; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.8e-95;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINQLLCKLPTDSELAPRSXCCHRLIFKGTSAITXCKENLPISLCSXQGLRAEN 60
 DB 1 KRCINQLLCKLPTDSELAPRSXCCHRLIFKGTSAITXCKENLPISLCSXQGLRAEN 60
 QY 61 ITESCQXRLPPAAXQISQOLIPTTEASASRXKXNQAKXEXPSN 103
 DB 61 ITESCQXRLPPAAXQISQOLIPTTEASASRXKXNQAKXEXPSN 103

RESULT 5
 ADF53279 ID ADF53279 standard; protein, 103 AA.
 AC ADF53279;
 XX 12-FEB-2004 (first entry)
 DT
 XX Human selenocysteine-containing selenoprotein P.
 DE
 XX anirrhematic; antiarthritic; rheumatoid arthritis; selenocysteine;
 KW selenoprotein P.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..103
 FT /note= "Xaa = selenocysteine"
 FT
 XX JP2003026598-A.
 PN
 XX 29-JAN-2003.
 PD
 XX 27-JUN-2001; 2001JP-00194617.
 PF
 XX 27-JUN-2001; 2001JP-00194617.
 PR
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 PA
 XX WPI; 2003-516438/49.
 DR
 XX New rheumatoid arthritis prevention and treating agent, containing
 PT selenoprotein P and its C terminal peptide; and diagnosis of rheumatoid
 PT arthritis.
 PT
 XX Disclosure; SEQ ID NO 1; 8pp; Japanese.
 PS
 XX The invention relates to a rheumatoid arthritis (RA) prevention and
 CC treating agent comprising a selenocysteine containing protein
 CC (selenoprotein P) and/or its C terminal peptide or peptide group
 CC consisting of its partial peptide as main constituents. The C terminal
 CC peptide or peptide group consisting of a partial selenoprotein P peptide
 CC derived from amino acids 260-362. The agent containing selenoprotein P
 CC and/or C terminal peptide or its peptide family is used for the
 CC prevention or treatment of RA. It is also used for the diagnosis of
 CC immuno abnormality. This sequence corresponds to the human selenoprotein
 CC P protein from which the agents are derived.
 CC
 XX Sequence 103 AA;
 SQ
 Query Match 91.3%; Score 94; DB 7; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.8e-95;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KRCINQLLCKLPTDSELA PRSXCHRHILFEKTSALTQCKENLP SLCSXQGLRAEEN 60
 DB 1 KRCINQLLCKLPTDSELA PRSXCHRHILFEKTSALTQCKENLP SLCSXQGLRAEEN 60
 OY 61 ITESQXRLPPAAXOISQOLIPTTEASASRXKXNOAKXKXEP SN 103
 DB 61 ITESQXRLPPAAXOISQOLIPTTEASASRXKXNOAKXKXEP SN 103
 RESULT 6
 ADO71758 ID ADO71758 standard; protein, 103 AA.
 XX
 AC ADO71758;
 XX
 DT 09-SEP-2004 (first entry)
 DE Human selenocysteine-containing protein SEQ ID NO:2.
 XX

KW human; selenocysteine; neurotransmission; vasotropic; muscular;
 KW neuroprotective; nootropic; gastrointestinal; ophthalmological;
 KW synapse formation; erectile dysfunction; myasthenia gravis;
 KW slow channel syndrome; congenital myasthenia; Lambert Eaton syndrome;
 KW Alzheimer's disease; dementia; spino-cerebellar degeneration;
 KW autonomic imbalance; cerebral-blood-flow insufficiency;
 KW gastrointestinal disease; glaucoma.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 22
 FT /note= "selenocysteine"
 FT Modified-site 40
 FT /note= "selenocysteine"
 FT Modified-site 52
 FT /note= "selenocysteine"
 FT Modified-site 67
 FT /note= "selenocysteine"
 FT Modified-site 74
 FT /note= "selenocysteine"
 FT Modified-site 89
 FT /note= "selenocysteine"
 FT Modified-site 91
 FT /note= "selenocysteine"
 FT Modified-site 98
 FT /note= "selenocysteine"
 FT Modified-site 100
 FT /note= "selenocysteine"
 FT
 XX WO2004050114-A1.
 PN
 XX 17-JUN-2004.
 PD
 XX 28-NOV-2003; 2003WO-JP015227.
 PF
 XX 29-NOV-2002; 2002JP-00348714.
 PR
 XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
 PA
 XX Kawamura R, Naruse T, Hirashima M, Kaminaka K, Matsuda J;
 FI Masada H, Noda M, Wada K;
 PI
 XX WPI; 2004-461008/43.
 DR
 XX Novel agent comprising selenocysteine-containing protein capable of
 PT enhancing synapse formation, useful for improving neurotransmission
 PT failure such as myasthenia gravis or Alzheimer's disease.
 PT
 XX Disclosure; SEQ ID NO 2; 31pp; Japanese.
 PS
 XX The invention relates to a novel agent for improving neurotransmission
 CC failure, comprising selenocysteine-containing protein (seleno protein P).
 CC An agent of the invention has vasotropic, muscular, neuroprotective,
 CC nootropic, gastrointestinal, and ophthalmological activity, and acts as
 CC an enhancer of synapse formation. The agent is useful for treating
 CC neurotransmission failure such as erectile dysfunction, myasthenia
 CC gravis, slow channel syndrome, congenital myasthenia, Lambert Eaton
 CC syndrome, Alzheimer's disease, dementia, spino-cerebellar degeneration,
 CC autonomic imbalance, cerebral-blood-flow insufficiency, gastrointestinal
 CC disease or glaucoma. The present sequence represents a selenocysteine-
 CC containing protein of the invention.
 XX
 SQ Sequence 103 AA;

Query Match 91.3%; Score 94; DB 8; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.8e-95;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KRCINQLLCKLPTDSELA PRSXCHRHILFEKTSALTQCKENLP SLCSXQGLRAEEN 60
 DB 1 KRCINQLLCKLPTDSELA PRSXCHRHILFEKTSALTQCKENLP SLCSXQGLRAEEN 60

QY 61 ITESCQXRLPPAAQISOQLIPTASASXRXKNQAKCXKXPSN 103
 DB 61 ITESCQXRLPPAAQISOQLIPTASASXRXKNQAKCXKXPSN 103

RESULT 7

ADP90528
 ID ADP90528 standard; protein; 103 AA.

AC ADP90528;

DT 23-SEP-2004 (first entry)

DE C-terminal human seleno protein P SeqID 2.

XX human; seleno protein P; inflammatory disease; interleukin-6; IL-6;
 KW systemic inflammatory response syndrome; thermal burn;
 KW acute pancreatitis; peritonitis; inflammatory bowel disease;
 KW organ fibrosis; malignant tumour; infectious disease; sepsis;
 KW disseminated intravascular coagulation syndrome; cell death inhibitor;
 KW antiinflammatory; vulnery; cytostatic; antimicrobial; antibacterial;
 KW immunosuppressive; anticoagulant.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..103

FT /label= Xaa

FT /note= "Xaa= selenocysteine"

PN JP2004182683-A.

XX 02-JUL-2004.

XX 05-DEC-2002; 2002JP-00354122.

XX 05-DEC-2002; 2002JP-00354122.

PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX WPI; 2004-473047/45.

XX Novel inflammatory disease-improving agent having seleno cysteine-
 PT containing peptide, seleno cysteine-containing protein and/or its
 PT peptide, useful for treating systemic inflammatory response syndrome.

PS Disclosure; SEQ ID NO 2; 16pp; Japanese.

XX This invention relates to a novel seleno cysteine containing peptide that
 CC can used to treat an inflammatory disease associated with interleukin-6
 CC (IL-6) production. Specifically, it refers to a peptide that can inhibit
 CC IL-6 production that is associated with systemic inflammatory response
 CC syndrome. The present invention describes the development of
 CC pharmaceutical compositions derived from this seleno cysteine containing
 CC protein or peptide that can therefore be used for treating inflammatory
 CC diseases of external injury, thermal burns, surgical operation, and for
 CC treating acute pancreatitis, peritonitis, inflammatory bowel disease,
 CC organ fibrosis, malignant tumour, infectious disease, sepsis, systemic
 CC inflammatory response syndrome or disseminated intravascular coagulation
 CC syndrome. Accordingly, they are inhibitors of cell death and exhibit
 CC antiinflammatory, vulnery, cytostatic, antimicrobial, antibacterial,
 CC immunosuppressive and anticoagulant activities. This polypeptide sequence
 CC is the C-terminal human seleno protein P of the invention.

XX Sequence 103 AA;

Query Match 91.3%; Score 94; DB 8; Length 103;

Best Local Similarity 100.0%; Pred. No. 1.8e-95;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINQLCKLPTDSELAPRSXCCHRLIFKGTSAITXCKENLPSLCSXQGLRAEN 60

DB 1 KRCINQLCKLPTDSELAPRSXCCHRLIFKGTSAITXCKENLPSLCSXQGLRAEN 60

QY 61 ITESCQXRLPPAAQISOQLIPTASASXRXKNQAKCXKXPSN 103
 DB 61 ITESCQXRLPPAAQISOQLIPTASASXRXKNQAKCXKXPSN 103

RESULT 8

ADO71757

ID ADO71757 standard; protein; 362 AA.

AC ADO71757;

DT 09-SEP-2004 (first entry)

DE Human selenocysteine-containing protein SEQ ID NO:1.

XX human; selenocysteine; neurotransmission; vasotropic; muscular;
 KW neuroprotective; nootropic; gastrointestinal; ophthalmological;
 KW synapse formation; erectile dysfunction; myasthenia gravis;
 KW slow channel syndrome; congenital myasthenia; Lambert Eaton syndrome;
 KW Alzheimer's disease; dementia; spino-cerebellar degeneration;
 KW autonomic imbalance; cerebral-blood-flow insufficiency;
 KW gastrointestinal disease; glaucoma.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 40

FT /note= "selenocysteine"

FT Modified-site 281

FT /note= "selenocysteine"

FT Modified-site 299

FT /note= "selenocysteine"

FT Modified-site 311

FT /note= "selenocysteine"

FT Modified-site 326

FT /note= "selenocysteine"

FT Modified-site 333

FT /note= "selenocysteine"

FT Modified-site 348

FT /note= "selenocysteine"

FT Modified-site 350

FT /note= "selenocysteine"

FT Modified-site 357

FT /note= "selenocysteine"

FT Modified-site 359

FT /note= "selenocysteine"

XX WO2004050114-A1.

XX 17-JUN-2004.

XX 28-NOV-2003; 2003WO-JP015227.

XX 29-NOV-2002; 2002JP-00348714.

XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

XX Kawamura R, Naruse T, Hirashima M, Kaminaka K, Matsuda J;

XX Maeda H, Noda M, Wada K;

XX WPI; 2004-461008/43.

XX Novel agent comprising selenocysteine-containing protein capable of
 PT enhancing synapse formation, useful for improving neurotransmission
 PT failure such as myasthenia gravis or Alzheimer's disease.

PS Disclosure; SEQ ID NO 1; 31pp; Japanese.

XX The invention relates to a novel agent for improving neurotransmission
 CC failure, comprising selenocysteine-containing protein (seleno protein P).
 CC An agent of the invention has vasotropic, muscular, neuroprotective,
 CC nootropic, gastrointestinal, and ophthalmological activity, and acts as

CC an enhancer of synapse formation. The agent is useful for treating
 CC neurotransmission failure such as erectile dysfunction, myasthenia
 CC gravis, slow channel syndrome, congenital myasthenia, Lambert Eaton
 CC syndrome, Alzheimer's disease, dementia, spino-cerebellar degeneration,
 CC autonomic imbalance, cerebral-blood-flow insufficiency, gastrointestinal
 CC disease or glaucoma. The present sequence represents a selenocysteine-
 CC containing protein of the invention.

XX Sequence 362 AA;

Query Match 91.3%; Score 94; DB 8; Length 362;
 Best Local Similarity 100.0%; Pred. No. 5.9e-95;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINOLLCKLPTDSELA PRSXCHCHRLIPEKTSAITXCKENLPSLCSXQGLRAEEN 60
 DB 260 KRCINOLLCKLPTDSELA PRSXCHCHRLIPEKTSAITXCKENLPSLCSXQGLRAEEN 319
 QY 61 ITESQXRLPPAAQXISQOLIPTASASXRXKNQAKKXEP SN 103
 DB 320 ITESQXRLPPAAQXISQOLIPTASASXRXKNQAKKXEP SN 362

RESULT 9

ADP90527
 ID ADP90527 standard; protein; 362 AA.

XX ADP90527;

XX 23-SEP-2004 (first entry)

XX Human seleno protein P SeqID 1.

XX human; seleno protein P; inflammatory disease; interleukin-6; IL-6;
 KW systemic inflammatory response syndrome; thermal burn;
 KW acute pancreatitis; peritonitis; inflammatory bowel disease;
 KW organ fibrosis; malignant tumour; infectious disease; sepsis;
 KW disseminated intravascular coagulation syndrome; cell death inhibitor;
 KW antiinflammatory; vulnary; cytostatic; antimicrobial; antibacterial;
 KW immunosuppressive; anticoagulant.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Misc-difference 1..362
 FT /label= Xaa
 FT /note= "Xaa= selenocysteine"

XX JP2004182683-A.

XX 02-JUL-2004.

XX 05-DEC-2002; 2002JP-00354122.

XX 05-DEC-2002; 2002JP-00354122.

XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX WPI; 2004-473047/45.

XX Novel inflammatory disease-improving agent having seleno cysteine-
 PT containing peptide, seleno cysteine-containing protein and/or its
 PT peptide, useful for treating systemic inflammatory response syndrome.

PS Disclosure; SEQ ID NO 1; 16pp; Japanese.

XX This invention relates to a novel seleno cysteine containing peptide that
 CC can be used to treat an inflammatory disease associated with interleukin-6
 CC (IL-6) production. Specifically, it refers to a peptide that can inhibit
 CC IL-6 production that is associated with systemic inflammatory response
 CC syndrome. The present invention describes the development of
 CC pharmaceutical compositions derived from this seleno cysteine containing
 CC protein or peptide that can therefore be used for treating inflammatory

CC diseases of external injury, thermal burns, surgical operation, and for
 CC treating acute pancreatitis, peritonitis, inflammatory bowel disease,
 CC organ fibrosis, malignant tumour, infectious disease, sepsis, systemic
 CC inflammatory response syndrome or disseminated intravascular coagulation
 CC syndrome. Accordingly, they are inhibitors of cell death and exhibit
 CC antiinflammatory, vulnary, cytostatic, antimicrobial, antibacterial,
 CC immunosuppressive and anticoagulant activities. This polypeptide sequence
 CC is the human seleno protein P of the invention.

XX Sequence 362 AA;

Query Match 91.3%; Score 94; DB 8; Length 362;
 Best Local Similarity 100.0%; Pred. No. 5.9e-95;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINOLLCKLPTDSELA PRSXCHCHRLIPEKTSAITXCKENLPSLCSXQGLRAEEN 60
 DB 260 KRCINOLLCKLPTDSELA PRSXCHCHRLIPEKTSAITXCKENLPSLCSXQGLRAEEN 319
 QY 61 ITESQXRLPPAAQXISQOLIPTASASXRXKNQAKKXEP SN 103
 DB 320 ITESQXRLPPAAQXISQOLIPTASASXRXKNQAKKXEP SN 362

RESULT 10

AAU84306
 ID AAU84306 standard; protein; 381 AA.

XX AAU84306;

XX 08-MAY-2002 (first entry)

XX Human endometrial cancer related protein, SEPPI.

XX Human; endometrial cancer; differential expression; DNA microarray;
 KW protein microarray.

XX Homo sapiens.

XX WO200209573-A2.

XX 07-FEB-2002.

XX 31-JUL-2001; 2001WO-US024104.

XX 31-JUL-2000; 2000US-0221735P.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.

XX Mutter GL;

XX WPI; 2002-179967/23.

XX N-PSDB; ABK35526.

XX Diagnosing endometrial cancer comprises determining expression of nucleic
 PT acid molecules or expression products that are differentially expressed
 PT in normal and malignant endometrium.

XX Claim 33; Page 223-224; 233pp; English.

XX The invention relates to diagnosing endometrial cancer in a subject
 CC suspected of having endometrial cancer comprising determining the
 CC expression of a set of nucleic acid molecules or expression products in
 CC an endometrial sample suspected of being cancerous, where the set of
 CC nucleic acid molecules comprises at least 2 nucleic acid molecules
 CC selected from 50 fully defined sequences as given in the specification.
 CC The nucleic acids are used as an array of at least 2 of the 50 nucleic
 CC acids bound to a solid substrate. Also included is a solid-phase protein
 CC microarray comprising at least 2 antibodies or its antigen binding
 CC fragments, that specifically bind at least 2 different polypeptides from
 CC the 50 fully defined sequences as given in the specification, fixed to a
 CC solid substrate. The methods and arrays are useful for the diagnosis of
 CC endometrial cancer, selecting and monitoring treatment regimes and

CC identification of lead compounds useful for the treatment of endometrial
 CC cancer. The present sequence is one of 50 proteins differentially
 CC expressed between cancerous and non-cancerous samples
 XX
 SQ Sequence 381 AA;

Query Match 91.3%; Score 94; DB 5; Length 381;
 Best Local Similarity 100.0%; Pred. No. 6.2e-95;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINQLLCKLPTDSELA PRSKCHCHRLI FEKTSAITXCKENLPSLCSXQGLRAEN 60
 DB 279 KRCINQLLCKLPTDSELA PRSKCHCHRLI FEKTSAITXCKENLPSLCSXQGLRAEN 338
 QY 61 ITESQXRLPPAAQXISQOLIPTASASRXKKNQAKKXEP SN 103
 DB 339 ITESQXRLPPAAQXISQOLIPTASASRXKKNQAKKXEP SN 381

RESULT 11

ABU89753
 ID ABU89753 standard; protein; 381 AA.

AC ABU89753;

DT 10-JUL-2003 (first entry)

DE Protein differentially expressed in cardiovascular disease #47.

KW Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;
 KW myocardial infarction; cardiact; antiarteriosclerotic; antianginal;
 KW gene therapy; differential gene expression.

OS Homo sapiens.

PN WO2003031650-A2.

XX 17-APR-2003.

PF 02-OCT-2002; 2002WO-EP011034.

PR 08-OCT-2001; 2001GB-00024145.

XX (FARB) BAYER AG.

PI Munnes M, Gehrmann M, Wick M, Schmitz G;

DR WPI; 2003-403108/38.

DR N-FSDB; ACA89926.

PT Predicting, diagnosing or prognosing a cardiovascular disease, e.g.
 PT angina, ischemia, myocardial infarction or arteriosclerosis by detection
 PT of a polynucleotide in a biological sample comprises detecting a
 PT hybridization complex.

PS Claim 3; Page 391-392; 454pp; English.

XX The invention describes a method of predicting, diagnosing or prognosing
 CC a cardiovascular disease by detection of a polynucleotide in a biological
 CC sample comprises hybridising at least one of the polynucleotide to a
 CC nucleic acid material of a biological sample, thus forming a
 CC hybridisation complex, and detecting the hybridisation complex. The
 CC polynucleotides, polypeptides, antisense molecule, antibody and reagent
 CC are useful for preparing compositions for preventing, predicting or
 CC diagnosing, or a medicament for treating a cardiovascular disease, e.g.
 CC arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.
 CC This sequence represents a protein identified in the invention a being
 CC differentially expressed in individuals with cardiovascular disease

XX Sequence 381 AA;

Query Match 91.3%; Score 94; DB 6; Length 381;
 Best Local Similarity 100.0%; Pred. No. 6.2e-95;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPTDSELA PRSKCHCHRLI FEKTSAITXCKENLPSLCSXQGLRAEN 60
 DB 279 KRCINQLLCKLPTDSELA PRSKCHCHRLI FEKTSAITXCKENLPSLCSXQGLRAEN 338
 QY 61 ITESQXRLPPAAQXISQOLIPTASASRXKKNQAKKXEP SN 103
 DB 339 ITESQXRLPPAAQXISQOLIPTASASRXKKNQAKKXEP SN 381

RESULT 12

ABP55511
 ID ABP55511 standard; peptide; 33 AA.

XX AC ABP55511;

XX 18-FEB-2003 (first entry)

DE Human plasma selenoprotein P peptide SEQ ID NO:4.

KW Human; plasma; selenoprotein P; neurodegenerative disease;
 KW motor disorder; depression; nootropic; neuroprotective; anticonvulsant;
 KW cerebroprotective; aging; traumatic cerebrovascular damage; epilepsy;
 KW motorneuron disease.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Modified-site 22

FT /note= "selenocysteine"

XX WO200276492-A1.

PN 03-OCT-2002.

XX 31-AUG-2001; 2001WO-JP007525.

XX 23-MAR-2001; 2001JP-00084050.

XX (KAGA) CEMO-SERO-THERAPEUTIC RES INST.

PI Hirashima M, Sasaki T, Naruse T, Maeda H, Nozaki C;

XX WPI; 2003-058349/05.

XX Selenoprotein P-based novel remedies for ameliorating neurodegenerative
 PT diseases e.g. motor disorders including diseases associated with
 PT depression of motor function e.g. ageing, traumatic cerebrovascular
 PT damage and epilepsy.

XX Example 1; Page 11; 27pp; Japanese.

PS The present invention describes agents (I) for ameliorating motor
 CC disorders, containing as the main component selenoprotein P and/or its C-
 CC terminal peptides. (I) have nootropic, neuroprotective cerebroprotective
 CC and anticonvulsant activities. (I) can be used for ameliorating
 CC neurodegenerative diseases e.g. motor disorders including diseases
 CC associated with depression of motor function e.g. aging, traumatic
 CC cerebrovascular damage, epilepsy, motorneuron disease. The present
 CC sequence represents a human plasma selenoprotein P peptide which is used
 CC in the present invention

XX Sequence 33 AA;

Query Match 31.1%; Score 32; DB 6; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.8e-27;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINQLLCKLPTDSELA PRSKCHCHRLI FEK 33

DB 1 KRCINQLLCKLPTDSELA PRSKCHCHRLI FEK 33

RESULT 13
 ABP57373
 ID ABP57373 standard; peptide; 33 AA.
 XX
 AC ABP57373;
 XX
 DT 23-APR-2003 (first entry)
 XX
 DE Selenoprotein P related cytotoxicity inhibitory peptide SEQ ID NO:3.
 XX
 KW Cytotoxicity inhibitor; selenocysteine; selenoprotein P; human; plasma;
 KW nontropic; neuroprotective; antiarteriosclerotic; anti-HIV; AIDS;
 KW Alzheimer's disease; arteriosclerosis; cosmetic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 22
 FT /note= "selenocysteine"
 XX
 PN WO200292810-A1.
 XX
 PD 21-NOV-2002.
 XX
 PF 10-MAY-2002; 2002WO-JP004557.
 XX
 PR 11-MAY-2001; 2001JP-00141466.
 XX
 PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX
 PI Hirashima M, Naruse T, Maeda H, Nozaki C, Goto T, Akiyama K;
 PI Hattori W;
 XX
 DR WPI; 2003-129291/12.
 XX
 XX Screening of functional peptides with lower cytotoxicity than
 PT selenocysteine and cytotoxicity inhibitory activity, for use in drugs for
 PT diseases like Alzheimer's disease, AIDS and arteriosclerosis, and in
 PT cosmetics.
 XX
 PS Example 1; Page 15; 43pp; Japanese.
 XX
 CC The present invention describes peptides (I) comprising one or more
 CC selenocysteines that show lower cytotoxicity than selenocysteine and
 CC cytotoxicity inhibitory activity. Also described is a method for
 CC screening substances with cytotoxicity inhibitory activity by using the
 CC sudden cell death phenomenon in a cell culture system with an albumin or
 CC fatty acid-added serum-free medium for culturing a test substance, and
 CC evaluating the degree of cytotoxicity based on generation of peroxidised
 CC lipid, or glutathione peroxidase activity, as indication. (I) have
 CC nontropic, neuroprotective, antiarteriosclerotic and anti-HIV activities.
 CC The screened peptides are useful for drugs for diseases like Alzheimer's
 CC disease, AIDS and arteriosclerosis, and in cosmetics. The present
 CC sequence represents a selenoprotein P related peptide, which is used in
 CC an example from the present invention
 XX
 SQ Sequence 33 AA;
 XX
 Query Match 31.1%; Score 32; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.8e-27;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 KRCINQLLCKLPTDSELA PRSXCHCHRLIFEK 33
 Db 1 KRCINQLLCKLPTDSELA PRSXCHCHRLIFEK 33
 XX
 RESULT 14
 ABB99458
 ID ABB99458 standard; peptide; 33 AA.
 XX

AC ABB99458;
 XX
 DT 12-FEB-2003 (first entry)
 XX
 DE Amino acid sequence of a peptide derived from human selenoprotein P.
 XX
 KW Selenoprotein P; immunopathic disease; autoimmune disease;
 KW rheumatoid arthritis; multiple sclerosis; allergic disease;
 KW bronchial asthma.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 22
 FT /note= "selenocysteine"
 XX
 PN WO200276493-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 20-MAR-2002; 2002WO-JP002645.
 XX
 PR 23-MAR-2001; 2001JP-00084049.
 XX
 PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
 XX
 PI Hirashima M, Sasaki T, Naruse T, Maeda H, Nozaki C;
 PI WPI; 2003-058350/05.
 XX
 DR Selenoprotein P-derived novel drugs for preventing or treating
 PT immunopathic diseases including autoimmune diseases like rheumatoid
 PT arthritis and multiple sclerosis, and allergic diseases e.g. bronchial
 PT asthma.
 XX
 PS Example 1; Page 10; 26pp; Japanese.
 XX
 CC The present sequence represents a C-terminal peptide of selenoprotein P.
 CC The peptide is used in drugs for preventing/treating immunopathic
 CC diseases. The drugs are used for preventing or treating immunopathic
 CC diseases including autoimmune diseases like rheumatoid arthritis and
 CC multiple sclerosis, and allergic diseases e.g. bronchial asthma
 XX
 SQ Sequence 33 AA;
 XX
 Query Match 31.1%; Score 32; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.8e-27;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 KRCINQLLCKLPTDSELA PRSXCHCHRLIFEK 33
 Db 1 KRCINQLLCKLPTDSELA PRSXCHCHRLIFEK 33
 XX
 RESULT 15
 ADO71759
 ID ADO71759 standard; peptide; 33 AA.
 XX
 AC ADO71759;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human selenocysteine-containing peptide SEQ ID NO:3.
 XX
 KW human; selenocysteine; neurotransmission; vasotropic; muscular;
 KW neuroprotective; nontropic; gastrointestinal; ophthalmological;
 KW synapse formation; erectile dysfunction; myasthenia gravis;
 KW slow channel syndrome; congenital myasthenia; Lambert Eaton syndrome;
 KW Alzheimer's disease; dementia; spino-cerebellar degeneration;
 KW autonomic imbalance; cerebral-blood-flow insufficiency;
 KW gastrointestinal disease; glaucoma.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Modified-site 22
 FT /note= "selenocysteine"
 XX
 XX WO2004050114-A1.
 PN 17-JUN-2004.
 XX
 XX 28-NOV-2003; 2003WO-JP015227.
 XX
 XX 29-NOV-2002; 2002JP-00348714.
 XX
 XX (KAGA) CEMO-SERO-THERAPEUTIC RES INST.
 XX
 XX Kawamura R, Naruse T, Hirashima M, Kaminaka K, Matsuda J;
 PI Maeda H, Noda M, Wada K;
 XX
 XX WPI: 2004-461008/43.
 XX
 XX Novel agent comprising selenocysteine-containing protein capable of
 PT enhancing synapse formation, useful for improving neurotransmission
 PT failure such as myasthenia gravis or Alzheimer's disease.
 XX
 XX Disclosure; SEQ ID NO 3; 31pp; Japanese.
 XX
 XX The invention relates to a novel agent for improving neurotransmission
 CC failure, comprising selenocysteine-containing protein (seleno protein P).
 CC An agent of the invention has vasotropic, muscular, neuroprotective,
 CC nootropic, gastrointestinal, and ophthalmological activity, and acts as
 CC an enhancer of synapse formation. The agent is useful for treating
 CC neurotransmission failure such as erectile dysfunction, myasthenia
 CC gravis, slow channel syndrome, congenital myasthenia, Lambert Eaton
 CC syndrome, Alzheimer's disease, dementia, spino-cerebellar degeneration,
 CC autonomic imbalance, cerebral-blood-flow insufficiency, gastrointestinal
 CC disease or glaucoma. The present sequence represents a selenocysteine-
 XX containing peptide of the invention.
 XX
 XX Sequence 33 AA;
 XX
 XX Query Match 31.1%; Score 32; DB 8; Length 33;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e-27;
 XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 1 KRCINQLCKLPTDSELA PRSKCCHRLIFEK 33
 XX |||||
 XX Db 1 KRCINQLCKLPTDSELA PRSKCCHRLIFEK 33

Search completed: April 15, 2005, 10:26:22
 Job time : 172 secs

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OM protein - protein search, using sw model

Run on: April 15, 2005, 10:21:10 ; Search time 43 Seconds
(without alignments)
178.811 Million cell updates/sec

Title: US-09-856-199-3

Perfect score: 103

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Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA*

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- 3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	91.3	381	4 US-09-919-497-96	Sequence 96, Appl
2	21	20.4	110	4 US-09-513-999C-7836	Sequence 7836, Ap
3	7	6.8	240	4 US-09-270-767-44240	Sequence 44240, A
4	4	6.8	437	4 US-09-673-395A-579	Sequence 579, App
5	7	6.8	629	4 US-09-489-039A-9904	Sequence 9904, Ap
6	7	6.8	932	4 US-09-949-016-8989	Sequence 8989, Ap
7	6	5.8	64	4 US-09-248-796A-26135	Sequence 26135, A
8	6	5.8	70	4 US-09-248-796A-21825	Sequence 21825, A
9	6	5.8	102	4 US-09-621-976-6276	Sequence 6276, Ap
10	6	5.8	129	3 US-09-258-373-8	Sequence 8, Appl
11	6	5.8	137	4 US-09-248-796A-24602	Sequence 24602, A
12	6	5.8	138	4 US-09-248-796A-26039	Sequence 26039, A
13	6	5.8	140	3 US-08-930-894-4	Sequence 4, Appl
14	6	5.8	143	4 US-09-270-767-42631	Sequence 42631, A
15	6	5.8	159	4 US-09-248-796A-22420	Sequence 22420, A
16	6	5.8	162	4 US-09-270-767-38788	Sequence 38788, A
17	6	5.8	192	4 US-09-270-767-54005	Sequence 54005, A
18	6	5.8	193	4 US-09-252-991A-19226	Sequence 19226, A
19	6	5.8	199	4 US-09-902-540-10941	Sequence 10941, A
20	6	5.8	213	4 US-09-489-039A-11130	Sequence 11130, A
21	6	5.8	217	4 US-09-248-796A-22037	Sequence 22037, A
22	6	5.8	232	4 US-09-252-991A-20591	Sequence 20591, A
23	6	5.8	257	4 US-09-248-796A-19035	Sequence 19035, A
24	6	5.8	265	3 US-09-199-637A-369	Sequence 369, App
25	6	5.8	266	4 US-09-655-908-20	Sequence 20, Appl
26	6	5.8	273	4 US-09-270-767-40609	Sequence 40609, A
27	6	5.8	273	4 US-09-270-767-55825	Sequence 55825, A

28 6 5.8 278 4 US-09-248-796A-19983 Sequence 19983, A
29 6 5.8 297 4 US-09-252-991A-26587 Sequence 26587, A
30 6 5.8 301 4 US-09-502-540-12668 Sequence 12668, A
31 6 5.8 305 4 US-09-252-991A-23417 Sequence 23417, A
32 6 5.8 317 4 US-09-540-236-3125 Sequence 3125, Ap
33 6 5.8 320 4 US-09-270-767-34209 Sequence 34209, A
34 6 5.8 320 4 US-09-270-767-49426 Sequence 49426, A
35 6 5.8 325 4 US-09-543-681A-4269 Sequence 4269, Ap
36 6 5.8 326 4 US-09-252-991A-25474 Sequence 25474, A
37 6 5.8 327 4 US-09-252-991A-28744 Sequence 28744, A
38 6 5.8 334 4 US-09-547-435-8 Sequence 8, Appl
39 6 5.8 335 4 US-09-700-397-11 Sequence 11, Appl
40 6 5.8 339 4 US-09-328-352-7424 Sequence 7424, Ap
41 6 5.8 355 4 US-09-270-767-57489 Sequence 57489, A
42 6 5.8 355 4 US-09-248-796A-20711 Sequence 20711, A
43 6 5.8 359 3 US-09-150-133-11 Sequence 11, Appl
44 6 5.8 359 3 US-09-150-141-11 Sequence 11, Appl
45 6 5.8 359 3 US-09-374-493-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-919-497-96
; Sequence 96, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (59)..(59)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (300)..(300)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (318)..(318)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (330)..(330)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (345)..(345)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (352)..(352)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (367)..(367)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (369)..(369)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (376)..(376)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (378)..(378)
; OTHER INFORMATION: Xaa = any amino acid
US-09-919-497-96

Query Match 91.3%; Score 94; DB 4; Length 381;
Best Local Similarity 100.0%; Pred. No. 7.9e-96;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINQLLCKLPTDSELAPRSXCCHRHLPFKTGSATYQCKENLPSCSXQGLRAEEN 60
DB 279 KRCINQLLCKLPTDSELAPRSXCCHRHLPFKTGSATYQCKENLPSCSXQGLRAEEN 338
QY 61 ITESCOXRLPPAAXIOISQOLIPTESASXRXKNOAKKXEPSN 103
DB 339 ITESCOXRLPPAAXIOISQOLIPTESASXRXKNOAKKXEPSN 381

RESULT 2
US-09-513-999C-7836
; Sequence 7836, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7836
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24...-1
; OTHER INFORMATION: score 4.7
; OTHER INFORMATION: seq LLMIRSTAAATRS/SR

US-09-513-999C-7836

Query Match 20.4%; Score 21; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRCINQLLCKLPTDSELAPRS 21
DB 90 KRCINQLLCKLPTDSELAPRS 110

RESULT 3
US-09-270-767-44240
; Sequence 44240, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44240
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-44240

Query Match 6.8%; Score 7; DB 4; Length 240;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 QQLIPTE 84
DB 33 QQLIPTE 39

RESULT 4
US-09-673-395A-579
; Sequence 579, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 579
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-673-395A-579

Query Match 6.8%; Score 7; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LIPTAS 86
DB 34 LIPTAS 40

RESULT 5
US-09-489-039A-9904
; Sequence 9904, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9904
; LENGTH: 629
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-9904

Query Match 6.8%; Score 7; DB 4; Length 629;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LIPTAS 86
DB 251 LIPTAS 257

RESULT 6
US-09-949-016-8989
; Sequence 8989, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8989
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8989

Query Match 6.8%; Score 7; DB 4; Length 932;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 CKENLPS 48
Db 800 CKENLPS 806

RESULT 7

US-09-248-796A-26135
; Sequence 26135, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26135
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26135

Query Match 5.8%; Score 6; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 KNOAKK 97
Db 50 KNOAKK 55

RESULT 8

US-09-248-796A-21825
; Sequence 21825, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21825
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21825

Query Match 5.8%; Score 6; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 QOLIPT 83
Db 34 QOLIPT 39

RESULT 9

US-09-621-976-6276
; Sequence 6276, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6276
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 2
; OTHER INFORMATION: Xaa = *, Arg
; NAME/KEY: UNSURE
; LOCATION: 56
; OTHER INFORMATION: Xaa = Ala, Asp
; NAME/KEY: UNSURE
; LOCATION: 43
; OTHER INFORMATION: Xaa = Ala, Met, Thr, Val
; NAME/KEY: UNSURE
; LOCATION: 54
; OTHER INFORMATION: Xaa = Cys, Arg
; NAME/KEY: UNSURE
; LOCATION: 62
; OTHER INFORMATION: Xaa = Ile, Met, Thr
; NAME/KEY: UNSURE
; LOCATION: 59
; OTHER INFORMATION: Xaa = Leu, Pro
; NAME/KEY: UNSURE
; LOCATION: 48
; OTHER INFORMATION: Xaa = Leu, Ser
; NAME/KEY: UNSURE
; LOCATION: 55
; OTHER INFORMATION: Xaa = Phe, Leu, Pro, Ser
; NAME/KEY: UNSURE
; LOCATION: 67
; OTHER INFORMATION: Xaa = Pro, Arg
US-09-621-976-6276

Query Match 5.8%; Score 6; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LPSLCS 51
Db 4 LPSLCS 9

RESULT 10
US-09-258-373-8
; Sequence 8, Application US/09258373
; Patent No. 6150110
; GENERAL INFORMATION:
; APPLICANT: Fletcher, Jonathan A.
; APPLICANT: Xiao, Sheng
; TITLE OF INVENTION: HMGI(Y)-LAMA4* FUSION ONCOGENE,
; TITLE OF INVENTION: ONCOPROTEIN AND METHODS OF USE
; FILE REFERENCE: B0801/7135/ERP
; CURRENT APPLICATION NUMBER: US/09/258,373
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 60/076,401
; EARLIER FILING DATE: 1998-02-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-258-373-8

Query Match 5.8%; Score 6; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 RLPPAA 73
Db 59 RLPPAA 64

RESULT 11
US-09-248-796A-24602
; Sequence 24602, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24602
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24602

Query Match 5.8%; Score 6; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 KTGSAL 38
Db 81 KTGSAL 86

RESULT 12
US-09-248-796A-26039
; Sequence 26039, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26039
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26039

Query Match 5.8%; Score 6; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LCKLPT 13
Db 21 LCKLPT 26

RESULT 13
US-08-930-894-4
; Sequence 4, Application US/08930894
; Patent No. 6037524
; GENERAL INFORMATION:
; APPLICANT: GREENLAND, Andrew James
; APPLICANT: DRAPER, John
; APPLICANT: SKIPSEY, Marc
; APPLICANT: WARNER, Simon
; TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEIN HYDROLASE PROMOTER
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,894
; FILING DATE: 09-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00882
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507381.3
; FILING DATE: 10-APR-1995
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: ARABIDOPSIS SHH PROTEIN
US-08-930-894-4

Query Match 5.8%; Score 6; DB 3; Length 140;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 IFEKGT 35
Db 64 IFEKGT 69

RESULT 14

US-09-270-767-42631
 ; Sequence 42631, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 42631
 ; LENGTH: 143
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-270-767-42631

Query Match 5.8%; Score 6; DB 4; Length 143;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 LPSLCS 51
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 Db 71 LPSLCS 76

RESULT 15

US-09-248-796A-22420
 ; Sequence 22420, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 22420
 ; LENGTH: 159
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-09-248-796A-22420

Query Match 5.8%; Score 6; DB 4; Length 159;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 ISQQLI 81
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 Db 76 ISQQLI 81

Search completed: April 15, 2005, 10:31:08
 Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: April 15, 2005, 10:29:36 ; Search time 131 Seconds
(without alignments)
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Title: US-09-856-199-3
Perfect score: 103
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Gapop 60.0 , Gapext 60.0

Searched: 1421835 seqs, 332370683 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	91.3	103	17	US-10-472-444-3
2	94	91.3	381	9	US-09-919-497-96
3	32	31.1	33	17	US-10-472-444-4
4	28	27.2	29	17	US-10-472-444-1
5	26	25.2	28	17	US-10-472-444-2
6	21	20.4	21	17	US-10-472-444-5
7	21	20.4	240	9	US-09-925-300-1658
8	21	20.4	299	15	US-10-210-172-20
9	7	6.8	277	16	US-10-767-701-37978
10	7	6.8	305	14	US-10-106-698-6240
11	7	6.8	524	15	US-10-104-047-3318
12	7	6.8	559	9	US-09-801-368-256
13	7	6.8	614	15	US-10-282-122A-60130
					Sequence 3, Appli
					Sequence 96, Appl
					Sequence 4, Appli
					Sequence 1, Appli
					Sequence 2, Appli
					Sequence 5, Appli
					Sequence 1658, Ap
					Sequence 20, Appl
					Sequence 37978, A
					Sequence 6240, Ap
					Sequence 3318, Ap
					Sequence 256, App
					Sequence 60130, A

14	7	6.8	932	14	US-10-174-677-88	Sequence 88, Appl
15	6	5.8	32	16	US-10-437-963-113469	Sequence 113469,
16	6	5.8	34	15	US-10-424-599-244168	Sequence 244168,
17	6	5.8	42	15	US-10-424-599-240047	Sequence 240047,
18	6	5.8	44	16	US-10-437-963-189520	Sequence 189520,
19	6	5.8	51	9	US-09-764-860-327	Sequence 327, App
20	6	5.8	51	14	US-10-074-095-327	Sequence 327, App
21	6	5.8	51	15	US-10-212-872-327	Sequence 204167,
22	6	5.8	54	16	US-10-437-963-204167	Sequence 138211,
23	6	5.8	55	16	US-10-437-963-138211	Sequence 288, App
24	6	5.8	58	9	US-09-867-550-288	Sequence 39, Appl
25	6	5.8	58	17	US-10-488-197-39	Sequence 254734,
26	6	5.8	59	15	US-10-424-599-254734	Sequence 254734,
27	6	5.8	59	15	US-10-424-599-276714	Sequence 276714,
28	6	5.8	62	10	US-09-776-724A-148	Sequence 148, App
29	6	5.8	65	16	US-10-437-963-185369	Sequence 185369,
30	6	5.8	68	15	US-10-335-977-8824	Sequence 8824, Ap
31	6	5.8	71	15	US-10-282-122A-72703	Sequence 72703, A
32	6	5.8	71	15	US-10-282-122A-74878	Sequence 74878, A
33	6	5.8	71	15	US-10-282-122A-76246	Sequence 76246, A
34	6	5.8	73	15	US-10-424-599-254742	Sequence 254742,
35	6	5.8	74	15	US-10-424-599-179756	Sequence 179756,
36	6	5.8	75	15	US-10-424-599-269051	Sequence 269051,
37	6	5.8	77	9	US-09-815-242-13035	Sequence 13035, A
38	6	5.8	78	16	US-10-437-963-134304	Sequence 134304,
39	6	5.8	79	15	US-10-424-599-158448	Sequence 158448,
40	6	5.8	79	16	US-10-437-963-197766	Sequence 197766,
41	6	5.8	80	15	US-10-264-049-2304	Sequence 2304, Ap
42	6	5.8	82	11	US-09-833-245-1510	Sequence 1510, Ap
43	6	5.8	82	11	US-09-833-245-1511	Sequence 1511, Ap
44	6	5.8	82	11	US-09-833-245-1694	Sequence 1694, Ap
45	6	5.8	82	11	US-09-833-245-1695	Sequence 1695, Ap

ALIGNMENTS

RESULT 1
US-10-472-444-3
; Sequence 3, Application US/10472444
; Publication No. US20050037954A1
; GENERAL INFORMATION:
; APPLICANT: HIRASHIMA, Masaki et al.
; TITLE OF INVENTION: NOVEL MEDICAMENT FOR AMERLIORATING DYSKINESIA
; FILE REFERENCE: 0020-5180P
; CURRENT APPLICATION NUMBER: US/10/472.444
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: JP 2001-84050
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22)..(22)
; OTHER INFORMATION: Xaa represents selenocysteine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (40)..(40)
; OTHER INFORMATION: Xaa represents selenocysteine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (52)..(52)
; OTHER INFORMATION: Xaa represents selenocysteine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (67)..(67)
; OTHER INFORMATION: Xaa represents selenocysteine
; FEATURE:
; NAME/KEY: misc feature

; LOCATION: (74)...(74)
 ; OTHER INFORMATION: Xaa represents selenocysteine
 ; FEATURE:
 ; NAME/KEY: misc_feature
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 ; FEATURE:
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 ; LOCATION: (100)...(100)
 ; OTHER INFORMATION: Xaa represents selenocysteine
 ; US-10-472-444-3

Query Match 91.3%; Score 94; DB 17; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.3e-89;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPTDSELA PRSXCHCHRLIFETGSAITXQCKENLPSLCSXQGLRAEEN 60
 Db 1 KRCINQLLCKLPTDSELA PRSXCHCHRLIFETGSAITXQCKENLPSLCSXQGLRAEEN 60
 QY 61 ITESQXRLPPAAQISOQLIPTASASXRXKXNOAKKXEPSN 103
 Db 61 ITESQXRLPPAAQISOQLIPTASASXRXKXNOAKKXEPSN 103

RESULT 2
 US-09-919-497-96
 ; Sequence 96, Application US/09919497
 ; Patent No. US2002010662A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mutter, George L.
 ; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
 ; FILE REFERENCE: B0801/7225
 ; CURRENT APPLICATION NUMBER: US/09/919,497
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: US 60/221,735
 ; PRIOR FILING DATE: 2000-07-31
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 96
 ; LENGTH: 381
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (59)...(59)
 ; OTHER INFORMATION: Xaa = any amino acid
 ; NAME/KEY: UNSURE
 ; LOCATION: (300)...(300)
 ; OTHER INFORMATION: Xaa = any amino acid
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 ; LOCATION: (378)...(378)
 ; OTHER INFORMATION: Xaa = any amino acid
 ; US-09-919-497-96

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 Best Local Similarity 100.0%; Pred. No. 4.2e-89;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPTDSELA PRSXCHCHRLIFETGSAITXQCKENLPSLCSXQGLRAEEN 60
 Db 279 KRCINQLLCKLPTDSELA PRSXCHCHRLIFETGSAITXQCKENLPSLCSXQGLRAEEN 338
 QY 61 ITESQXRLPPAAQISOQLIPTASASXRXKXNOAKKXEPSN 103
 Db 339 ITESQXRLPPAAQISOQLIPTASASXRXKXNOAKKXEPSN 381

RESULT 3
 US-10-472-444-4
 ; Sequence 4, Application US/10472444
 ; Publication No. US20050037954A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HIRASHIMA, Masaki et al.
 ; TITLE OF INVENTION: NOVEL MEDICAMENT FOR AMERLIORATING DYSKINESIA
 ; FILE REFERENCE: 0020-5180P
 ; CURRENT APPLICATION NUMBER: US/10/472,444
 ; CURRENT FILING DATE: 2003-09-23
 ; PRIOR APPLICATION NUMBER: JP 2001-84050
 ; PRIOR FILING DATE: 2001-03-23
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 4
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (22)...(22)
 ; OTHER INFORMATION: Xaa represents selenocysteine
 ; US-10-472-444-4

Query Match 31.1%; Score 32; DB 17; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.2e-25;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRCINQLLCKLPTDSELA PRSXCHCHRLIFETGSAITXQCKENLPSLCSXQGLRAEEN 33
 Db 1 KRCINQLLCKLPTDSELA PRSXCHCHRLIFETGSAITXQCKENLPSLCSXQGLRAEEN 33

RESULT 4
 US-10-472-444-1
 ; Sequence 1, Application US/10472444
 ; Publication No. US20050037954A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HIRASHIMA, Masaki et al.
 ; TITLE OF INVENTION: NOVEL MEDICAMENT FOR AMERLIORATING DYSKINESIA
 ; FILE REFERENCE: 0020-5180P
 ; CURRENT APPLICATION NUMBER: US/10/472,444
 ; CURRENT FILING DATE: 2003-09-23
 ; PRIOR APPLICATION NUMBER: JP 2001-84050
 ; PRIOR FILING DATE: 2001-03-23
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 29

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Query Match      20.4%; Score 21; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 KRCINQLCKLPTDSELAPRS 21
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RESULT 7
US-09-925-300-1658
; Sequence 1658, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1658
; LENGTH: 240
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-925-300-1658

Query Match      20.4%; Score 21; DB 9; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      220 KRCINQLCKLPTDSELAPRS 240
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RESULT 8
US-10-210-172-20
; Sequence 20, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shinkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjal, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malvankar, Uriel

```

APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Alsobrook II, John
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-416 A
CURRENT APPLICATION NUMBER: US/10/210,172
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/309,501
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/323,994
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/373,814
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/310,951
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,544
PRIOR FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/313,201
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/312,892
PRIOR FILING DATE: 2001-08-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 327
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 20
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
US-10-210-172-20

Query Match 20.4%; Score 21; DB 15; Length 299;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRCINQLLCLPTDSELAPRS 21
Db 279 KRCINQLLCLPTDSELAPRS 299

RESULT 9
US-10-767-701-37978
Sequence 37978, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 37978
LENGTH: 277
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(277)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C42729_1.pap
US-10-767-701-37978

Query Match 6.8%; Score 7; DB 16; Length 277;

Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 LLCKLPT 13
Db 104 LLCKLPT 110

RESULT 10

US-10-106-698-6240
Sequence 6240, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 6240
LENGTH: 305
TYPE: PRT
ORGANISM: Homo sapiens
US-10-106-698-6240

Query Match 6.8%; Score 7; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 QGLRAEE 59
Db 32 QGLRAEE 38

RESULT 11

US-10-104-047-3318
Sequence 3318, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
FILE REFERENCE: HI-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3318
LENGTH: 524
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3318

Query Match 6.8%; Score 7; DB 15; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 LIPTAS 86
Db 119 LIPTAS 125

RESULT 12

US-09-801-368-256
Sequence 256, Application US/09801368

Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 256
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-256

Query Match 6.8%; Score 7; DB 9; Length 559;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LPTDSEL 17
Db 533 LPTDSEL 539

RESULT 13
US-10-282-122A-60130
; Sequence 60130, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 60130
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-60130

Query Match 6.8%; Score 7; DB 15; Length 614;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 LIPTAS 86
Db 236 LIPTAS 242

RESULT 14
US-10-174-677-88
; Sequence 88, Application US/10174677
; Publication No. US20030190704A1
; GENERAL INFORMATION:
; APPLICANT: Xie, Ting
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANCHORING STEM CELLS IN A MICROENVIRONMENT
; FILE REFERENCE: 40716(IP-012)
; CURRENT APPLICATION NUMBER: US/10/174,677
; CURRENT FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 88
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-677-88

Query Match 6.8%; Score 7; DB 14; Length 932;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 CKENLPS 48
Db 800 CKENLPS 806

RESULT 15
US-10-437-963-113469
; Sequence 113469, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 113469

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; LENGTH: 32
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_17253C.1.pap
US-10-437-963-113469

Query Match      5.8% Score 6; DB 16; Length 32;
Best Local Similarity 100.0%; Pred.No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 NLP SLC 50
Db 23 NLP SLC 28

Search completed: April 15, 2005, 10:42:22
Job time : 131 secs

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